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Metarhizium anisopliae
Metarhizium anisopliae
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Bukaryota; Ascomycotales;
Clavicipitaceae; Metarhizium.

Clavicipitaceae; Metarhizium.

Soreen; E. D. G. 14)
Soreen; C. Mathur, P. and St. Leger, R. J.

EST analysis of the insect pathogenic fungus Metarhizium anisopliae
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ273402 Atarhizium anisopliae ARSEF 2575 Metarhizium anisopliae CDNA clone Ma#948, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xrefe="taxon:5530"
/clone="Ma#948"
/clone lib="Metarhizium anisopliae ARSEF 2575"
/clone lib="Metarhizium anisopliae was grown on
insect cuticle for 24 hours. A cDNA library was
constructed in the unidirectional Lambda vector, Unizap"
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                                                                                                          117 AACAGCTGTTTCTTCCACGATCCA-----AATCAAGAGGTGGCGCTTTACCCGAAGGTT 170
                                                                                                                                                                  171 AACTATÄÄCCACCGCAAAATCGTGTCATTTGCCCGTGTGACTTCATCCGGGGGGATTAC 230
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                       GlybeuTyrGlyGlnGlyGlnValValAlaValAlaAspIhrGlybeuAspIhrGlyArg 37
                                                                               38 AsnAspSerSerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAlaLeuGly 57
                                                                                                                                       58 ArgThrAsnAsn------ 61
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                                                                                                                                                                                                                                                                   291 ĠŤŤĂTTAGTAACGACGGTAĀĀTGCCAAGTATAATGGTGTCGCCAAGGGGGGAAGATTTC
                                                                                                                                                                                                            Valleu------GlyAsnAlaLeuAsnLysGlyMetAlaProGlnAlaAsnLeuVal
                                                                                                                                                                                                                                                                                                                                                              LeuPheSerGlnAlaTrpAsnAlaGlyAlaArglleHisThrAsnSerTrpGlyAlaPro
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/strain="ARSEF 2575"
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University of Maryland
4112 Plant Sciences Bui
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2121 bp DNA linear GSS 13-DEC-2002 100023066-5726 Aspergillus terreus random genomic DNA clone library Aspergillus terreus genomic, genomic survey sequence.
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Aspergillus terreus
Eukaryota; Fungi, Ascomycota; Pezizomycotina, Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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651

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmania; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 665)

NIH-MGC Metry://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov, University of Iowa cDNA Library preparation: Dr. Jim. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mag-llnl.gov

mhi: Clone Distribution: MGC clone distribution information can be http://mag-llnl.gov
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/tissue_type="whole_brain"
/dev_stage="embryo 12.5dpc"
/lab_host="HHIOB (T1 phage resistant)"
/clone=lib="NHIH BMAP_FIO"
/clone=lib="NHIH BMAP_FIO"
/clone="Organ: Brain; Vector: pxx-Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pxx-Asc; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665 bp mRNA linear EST 26-JUL-2002
UT-M-FIO-byv-m-19-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:5702970 5', mRNA sequence.
BQ770462
EQ770462.1 GI:21978936
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194 lealaaspasnProasnHisIlealaGlnPheSerSerargGlyalaThrargaspGlyA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 laProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrS
                                                                      ---AlaproGly-ThrAlaLysAsnAlaI
                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 erMetAlaThrProlleValAlaGly 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db xref="taxon:10090"
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Mus musculus
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                      Askenazi, M., Driggers, E.M., Holtzman, D.A., Norman, T.C., Iverson, S. Zimmer, D.P., Boers, M.E., Blomquist, P.R., Martinez, E.J., Sykes, K., Monrall, A.W., Feibelman, T.P., Mayorga, M.E., Maxon, M.E., Sykes, K., Tobin, J., Cordero, E., Salama, S.R., Trueheart, J., Royer, J.C. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Aspergillus terreus random genomic DNA clone library".
                                                                                                                                                    Integrating transcriptional and metabolite profiles to direct the engineering of lovastatin-producing strains Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pZErOTW-2; Site 1: Sau3A; Site 2: BamHI; Sau3A genomic fragments ligated into BamHI digested pZErOTM-2 "
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/strain="ATMC 20642 (A. terreus Thom, anamorph)"
/db.rref="taxon:33178"
/lab_host="Escherichia coli"
                                                                                                                                                                                                                                                                                           Cambridge, MA 02139,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Aspergillus terreus"
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Tel: 617-621-8322
Fax: 617-
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Madden, Κ.Τ.
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with EcoR I adaptor, digested with NotI and then cloned directionally into pyr.Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Matches:
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182.50
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                         /mol type="genomic DNA"
/strain="ATCC 49239"
/db.xref="taxon:224"
/clore lib="H1 pUC18 Library"
/note="Vector: pUC18; Site 1: Smal; A shotgun library
constructed from Halorubrum lacusprofundi genomic DNA
using pUC18/Smal/BAP plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::
536 GGAATGGAACACGCGACGAACGACGACGACGTGCTTCAGATGAGCCTCGGTGCG
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                                                                                                           Deutsch, K.,
                                            Archaea; Buryarchaeota; Halobacteria; Halobacteriales; Archaea; Buryarchaeota; Halobacteriaceae; Halobacteriaceae; Halobacteriaceae; Halobacea; Lo. 716)
Goo, Y., Roach, J., Glusman, G., Baliga, N.S., Deutsch, K., DasSarma, S., Ng, W.V. and Hood, L.
Low-pass Sequencing for Microbial Comparative Genomics Unpublished (2003)
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71
34
66
61
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1. 716
/organism="Halorubrum lacusprofundi"
                                                                                                                                                                                                               98103,
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                               Halorubrum lacusprofundi
 GI:33343985
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BZ893395 716 bp DNA linear GSS 30-JUL-2003 HLZ 0177 Hl pUC18 Library Halorubrum lacusprofundi genomic 5', genomic survey sequence.

Search completed: April 4, 2004, 11:54:47 Job time : 2284.58 secs

us-09-985-689a-4.rst

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92 Db

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716 bp DNA linear GSS 30-JUL-2003
HL2_0177 Hl pUC18 Library Halorubrum lacusprofundi genomic 5',
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 AACTATAACCACCGCAAAATCGTGTCATTTGCCCCGTGTGACTTCATCCGGGGGGATTAC 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 LeuPheSerGinAlaTrpAsnAlaGlyAlaArgileHisThrAsnSerTrpGlyAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 ValAsnGlyAlaTyrThrAlaAsnSerArgGlnValAspGluTyrValArgAsn---Asn
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Halorubrum lacusprofundi
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halorubrum.
1 (bases I to 716)
Goo, Y., Roach, J., Glusman, G., Baliga, N.S., Deutsch, K.,
DasSarma, S., Ng, W.V. and Hood, L.
Low-pars Sequencing for Microbial Comparative Genomics
Unpublished (2003)
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1441 North 34th Street, Seattle, WA
Tel: 206 732 1412
Fax: 206 732 1299
Email: ygoodsystemsbiology.org
Seq primer: Ml3 Forward
Class: shotgun.
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                                         9.18e-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nhi@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Data to a cloned population of
Trypanosoma brucei (TREU927/4 Gurat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smitch, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing small
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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I (bases 1 to 574)

I (bases 1 to 574)

Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        255
                                                                                       136 AlaTyrThrAlaAsnSerArgGlnValAspGluTyrValArgAsnAsnAspMetThrVal 155
                                                                                                                  LeuPheAlaAlaGlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAla 175
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                                           ------ĠĠŢ 331
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Trypanosoma brucei
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae,
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                             284 ACCCGCGGCTGCCCCAACGGCGCCATTGCTTCCATGAGCCTGGGA-
                                                                                                                                                                                                                                                                                                   +49 CCTTCTGCCTGCACTGTTGGTGCCTCT-----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
AL490202
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119 AsnAlaGly
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LOCUS DEFINITION

RESULT 13 TA315H10P

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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

ACCESSION VERSION KEYWORDS SOURCE

290

75

470

Deutsch, K., Pan, M.,

Location/Qualifiers

FEATURES

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organism="Mus musculus"
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IMAGE:5702970 5', mRNA sequence.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6"
                                                         Mus musculus (house mouse)
Mus musculus
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BQ770462.1 GI:21978936
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UI-M-FIO-byv-m-19-0-UI.:1 NIH_BMAP_FIO Mus musculus cDNA clone
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                                                          /db_xref="taxon:2247"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yThrAlaLysAsnAlaIleThrValGlyAlaThrGluAsnTyrArgProSerPheGlySe 193
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                'organism="Halorubrum lacusprofundi"
|mol_type="genomic DNA"
|strain="ATCC 49239"
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Matches:
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/db xref="taxon:10090"
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/dlone="MAGE:5702270"
/tissue_type="whole brain"
/dev stage="embryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
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/clone=1bh="NH1E BMAP [F10"
/clone=1bh="NH1E BMAP [F10"
/clone=10rgan: Brain; Vector: ptx- Asc; Site_1: EcoR I;
/clone=10rgan: Brain; Vector: ptx- Asc; Vector: ptx- A
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 665)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspProAsnGlyHisGlyThrHisValAlaGlySerValLeuGlyAsnAlaLeuAsnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 GlyMetAlaProGlnAlaAsnLeu---ValPheGlnSerlleMetAspSerSerGlyGly
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Matches:
Conservative:
Mismatches:
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161 AsnGludiyProAsnSerdiyThrIleSerAlaProGlyThrAlaLysAsnAlaIleThr 180
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                                                                                                                                                                                                     356 GIGGGIGGC-----ATTGACTTTGAAGATAAC 382
                                                                                                                                                                                                                                                                                                                                                                                   -------TCCGGTGTGAAAGGGGGCTGCCGTGCACTCTCAGGGACCAGT 526
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123 ArgileHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsnSerArg 142
                       176 CTAAAGAAGATGGACGTTCTCAACCTTAGCATCGGTGGGCCCCGACTTCATGGATCATCCG 235
                                                        143 GlnValAspGluTyr-----ValArgAsnAsnAspMetThrValLeuPheAlaAlaGly 160
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Search completed: April 4, 2004, 11:54:55 Job time : 2282.58 secs

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ABO46402 Bacillus
ED3808 DNA encodin
ABO46404 Bacillus
ABO66404 Bacillus
ABO662155 Nucleic a
ABO64155 Sequence
AR364155 Bacillus
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AR017218 Geobacter
UG0086 Dictyosteli
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AR00309 Thermoana
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AR20331 Streptomy
AR44556 Streptomy
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AL939105 Streptomy
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-UNITS=bits -SPART=1 -END=-1 - MATRIX=100000000
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1 NDVARGIVKADVAQNNYGLY......EVQAYNVPSGPQRFSLAIVH 433
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
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LeuAsnLysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSerSer
                                                  GlyAlaArg1leHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsn
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Saeki,K., Okuda,M., Hatada,Y., Kobayashi,T., Ito,S., Takami,H. an Morikoshi,K.
Novel oxidatively stable subtilisin-like serine proteases from alkaliphilic Bacillus spp.: enzymatic properties, sequences, and elvaliphilic Bacillus spp.: enzymatic properties, sequences, and blochem. Biophys. Res. Commun. 279 (2), 313-319 (2000)
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Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Biological Science Laboratory; Ichikaimachi Akabane 2606, 1
Tochigi 321-3497, Japan (B-mail:3871855kastanet.kao.co.jp,
Tel:81-285-68-7400, Fax:81-285-68-7403)
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                                                 LeuAsnLysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSerSer
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Seath, K., Okuda, M., Hatada, Y., Kobayashi, T., Ito, S., Takami, H. and Horikoshi, K.
Novel oxidatively stable subtilisin-like serine proteases from alkaliphilic Bacillus spp.: enzymatic properties, sequences, and evolutionary relationships
Biochem. Biophys. Res. Commun. 279 (2), 313-319 (2000)
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Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Biological Science Laboratory, Ichikaimachi Akabane 2606, Haga,
Tochigi 321-3497, Japan (E-mail:387186@kastanet.kao.co.jp,
Tel:81-285-68-7400, Fax:81-285-68-7403)
Location/Qualifiers
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                                                                    GlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAla
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/organism="Bacillus sp."
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Saeki, K., Okuda, M., Hatada, Y., Kobayashi, T., Ito, S., Takami, H. i
Horikoshi, K.
Novel oxidatively stable subtilisin-like serine proteases from
alkaliphilo Bacillus spp.: enzymatic properties, sequences, an
evolutionary relationships
Biochem. Biophys. Res. Commun. 279 (2), 313-319 (2000)
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Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Biological Science Laboratory; Ichikaimachi Akabane 2606, l
Tochigi 321-3497, Japan (E-mail:3871856kastanet.kao.co.jp,
Tel:81-285-68-7400, Jax:81-285-68-7403)
                           BCT
                                                                              AB046404 1 Inear 1299 bp DNA linear Bacillus sp. Y PROC gene for protease, partial cds. AB046404.1 GI:12381940
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Saeki, K.
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Nucleic acids encoding a polypeptide having protease activity.

Nucleic acids encoding a polypeptide having protease activity.

BD062155.1

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GI:22607760

S D 2001514529-4/39.

Homo sapiens (human)

ISM Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

BUKARYOCTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

S Sloma, A. and Christianson, L.

Nucleic acids encoding a polypeptide having protease activity

AL Patent: JP 2001514529-A/39

PD 11-SEP-2001;

NOVO NORDISK BIOTECH INC

PN UP 2001514529-A/39

PP 12-JUN-1999 UP 1999503145

PR 12-JUN-1997 US 08/873479

PI ALAM SLOMA, LYNNE CRRISTIANSON

PC C12N15/57, C12N15/75, C12N9/54, C12K14/00

CC Strandedness: Single;

CC Topology: Linear;
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Slowd. A. and Christianson, L.
Nucleic acids encoding a polypeptide having protease activity
Patent: US 5891701-A 41 06-APR-1999;
Patent: US 5891701-A 41 06-APR-1999;
Location/Qualifiers
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(sites)
Saeki,K., Okuda,M., Hatada,Y., Kobayashi,T., Ito,S., Takami,H. and Horikoshi,K.
Novel oxidatively stable subtilisin-like serine proteases from alkaliphilic Bacillus spp.: enzymatic properties, sequences, and evolutionary relationships
Biochem. Biophys. Res. Commun. 279 (2), 313-319 (2000)
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Stati, K.
Direct Submission
Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Submitted (20-JUL-2000) Lohikaimachi Akabane 2606, Haga,
Biological Science Laboratory; Ichikaimachi Akabane 2606,
Tochigi 321-3497, Japan (E-mail:387185@kastanet.kao.co.jp,
Tochigi 321-3490, Fax:81-285-68-7403)
Tel:81-285-68-7400, Fax:81-285-68-7403)
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Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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Valalagiyasnvalalaginleuarggiuhispheilelysasnarggiyilethippo
                                                                                                           bedda,M., Saeki,K. and Kobayashi,T.
Bacillus sp. KSM-9865 protease gene
Published Only in Database (2003)
2 (bases I to 1923)
Okuda,M., Saeki,K. and Kobayashi,T.
Direct Submission
Submitted (18-AR-2002) Mitsuyoshi Okuda, Kao corporation,
Biological Science Laboratory; Ichikaimachi Akabane 2606, He
Tochigi 321-3497, Japan (E-mail:okuda.mitsuyoshi@kao.co.jp,
Tel:81-285-68-7543, Fax:81-285-68-7547)
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Bacillus sp. KSM-9865
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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protease,
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Bacillus sp. KSM-9865 gene for I
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AQSSYGLYGQGQIVAVADTGLDTGRNDSSMHBAFRGKITALYALGRTNNANDTNGHGT
THYGGSYLGROSGTNKGNAAPQALLYFOGIMDSGGGLGGLPSNIQTESQSYSGARIHTN
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GOGGNGRVATTLDKSLNNAYVNESSSLSTSGKATYSFTATAGKPIKISLVWSDAPASTTA
SVTLVNDLDDLVITTARGLNVAYVNESSSLSTSGKATYSFTATAGKPIKISLVWSDAPASTTA
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Novel oxidatively stable subtilisin-like serine proteases from alkaliphilic Bacillus spp.: enzymatic properties, sequences, and evolutionary relationships
Biochem. Blophys. Res. Commun. 279 (2), 313-319 (2000)
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Submitted (20-JUL-2000) Katsuhisa Saeki, Kao corporation,
Biological Science Laboratory, Ichikaimachi Akabane 2606,
Tochigi 321-3497, Japan (E-mail:38718980kastanet.kao.co.jp,
Tel:81-285-68-7400, Fax:81-285-68-7403)
On May 9, 2002 this sequence version replaced gi:12381938.
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Bacillus sp. 9860
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Bacillus sp. 9860 PROA gene for
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AB046403.2 GI:20521152
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LysproserteullelysAlaAlaLeulleAlaGlyAlaThrAspValGlyLeuGlyTyr 299
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S Takaiwa,M., Okuda,M., Saeki,K., Kubota,H., Hit Shikata,S. and Nomura,M.
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Sequence 3 from patent US 6376227.
AR368116 GI:34601777
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979 GCTGGTGCCAGAATTCATACAAACTCCTGGGGAGCAGCAGTGAATGGGGCTTACACAACA 1038
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SEQUENCE 2 from Patent EP1347044.

DEFINITION Sequence 2 from Patent EP1347044.

DEFINITION AX839476
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Okuda,M.K., Sato,T.K., Saito,K.K., Sumitomo,N.K., Izawa,Y.K., Saeki,K.K., Kobayashi,T.K. and Nomura,M.K. Alkaline protease
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Matches:
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Direct Submitssion

Submitted (21-NOV-2000) Katsuhisa Saeki, KAO, CORPORATION, 2606, AKABANE, ICHIKAIMACHI, HAGA, TOCHIGI 321-3486, Japan (E-mail:38714856ksatanet.kao.co.jp, Tel:81285687471(ex.7471), Eax.81285687403)

On May 9, 2002 this sequence version replaced gi:14164344.
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Bacillus sp. KSM-KP43
Bacteria; Firmicutes; Bacillales; Bacillus
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Bacillus sp. KP43 PROF 9
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ORIGIN	Alignment Scores: 3.17e-11. Pred. No.: 3.17e-11. Score: 1999.50 Percent Similarity: 94.24% Best Local Similarity: 87.79% Query Match: 6	US-09-985-689A-5 (1-433) x AR368 Qy 1 AshAspValAlaArgGly	Db 619 AATGATGTTGCGCGTGGA  21 GlyGlnGlyGlnValVal	Db 679 GGACAGGACAGATCCTIA  Qy 41 SerMetHeGLUAlaPher	Db 739 TCGATGAAGAAGCTTC	Db 799 AAIGCCAAIGAIACGAAR Qy 80 AlaLeuasnLysGlyMet.	859	919	979	1039	1099	1159	Db 1219 CATGTGGCACAGTTCTCT  Qy 220 ThralaproGlyThrphe	Db 1279 ATGGCACCGGGAACGTTC	Qy 240 TrplaasnTyrAsnSer         :::::    	Qy 260 ValAlaGlyAsnValAla 		Db 1459 AAGCCTTCTCTATTAAAA 300 ProSerGlyAspGlnGly
Db 1099 GGGAATGAAGGACCGAACGGGGGAACCATCAGTGCACCAGGCACAGCTAAAAATGCAATA 1158	Qy         180 ThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsn 199           Db         1159 ACAGTGGAAGTTACGGAAAACCTCCGCCCAAGCTTTGGGTCTTATGCGACAATATCAAC 1218           Qy         200 HisIleAlaGlnPheSerSerArgGlyAlaThrArgAspGlyArgIleLysProAspVal 219           Db         1219 CATGTGGCACAGTTCTCTTCACGTGGACCGACAAAGGATGAACGGATCAAACCGGATGTC 1278	Qy 220 ThralabrodlyThrPheileteuSerAlaArgSerSerLeuAlaBroAspSerSerPhe 239	Qy 240 TrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrSerMetAlaThrProlle 259	Qy 260 ValalaGlyAsnValalaGlnLeuArgGluHisPhelleLySAsnArgGlyIleThrPro 279	Cy 280 LysProSerbeulleLysAlaAlaLeulleAlaGlyAlaThrAspValGlyLeuGlyTyr 299	Oy 300 ProserGlyAspGlnGlyTrpGlyArgValThrLeuAspLy8SerLeuAsnValAlaTyr 319	Qy 320 ValasnGlualarhralaLeualaThrGlyGlnLysAlaThrTyrSerPheGlnalaGln 339	340 AladlyLysProLeuLysIleSerLeuValTrpThrAspAlaProGlySerThrThrAla 359 1639 GCGGCAAGCCTTTGAAATCTCCCTGGAATGGCCCTGCCAGGCAAACGT 169	Oy 360 SerTyrThrLeuValAsnAspLeuAspLeuVallleThrAlaProAsnGlyGlnLysTyr 379	Oy 380 ValGlyasnaspPheSerTyrProTyraspAsnasnTrpaspGlyargasnasnValGlu 399	Oy 400 AsnValPheileAsnAlaProGlnSerGlyThrTyrThrIleGluValGlnAlaTyrAsn 419 Db 1819 AATGTATTAATGACACCACAAAGCGGGACGTATACAATTGAGGTACAGGTTATAAC 1878	Qy 420 ValProSerGlyProGlnArgPheSerLeuAlaileValHis 433		sequence > irom patent US e AR368117 AR368117.1 GT:34601778	Unknown.	REFERENCE 1 (bases to 1923) AUTHORS Takaiwa,M., Okuda,M., Saeki,K., Kubota,H., Hitomi,J., Kageyama,Y., Shikata,S. and Nomura,M.	TITLE Alkaline proteases 23-APR-2002; JOURNAL Patent: US 6376227-8 5 23-APR-2002; FEATURES	Source

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Matches:
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uncultured marine group II euryarchaeote 37F11
Archaea: Euryarchaeota; Marine Group II; environmental samples.
I (bases 1 to 60006)
Beja.C., Suzuki,M.T., Koonin,E.V., Aravind,L., Hadd,A.,
Nguyen,L.P., Villacorta,R., Amjadi,M., Garrigues,C.,
Jovanovich,S.B., Feldman,R.A. and Delong,E.F.
Construction and analysis of bacterial artificial chromosome libraties from a marine microbial assemblage
Environ. Microbiol. 2 (5), 516-529 (2000)
                                                                                                                                                                                                                                                                     AlaGlyLysProLeuLysIleSerLeuValTrpThrAspAlaProGlySerThrThrAla
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Beja.O., Suzuki, M.T., Koonin, E.V., Aravind, L., Hadd, A., Nguyen, L.P., Villacorta, R., Amjadi, M., Garrigues, C., Nguyen, L.P., Villacorta, R.A. and Delong, E.F.
Direct Submission
Submitted (17-MAY-2000) R. E. D. Monterey Bay Aquarium Research Institute, P.O. Box 628, Moss Landing, CA 95039-0628, USA Location/Qualifiers
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16718 ATTGGTACTCACTCAAATGGTCGTTCAATGTATATGCAACTCAGCGGAACTTCTCAAGCA 16659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACGGTATICTOTTCTGCACGAGGAAGCAAGAACGTTGTTGGTTCAGTCTGCGGT 16719
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17041 AATGCATGGGGTCTTAATGGAATTACGGAGCCTACACTGCTGA-TCAGATCGACAGAT 16983
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17383 GCTCCTTCTTCTAAATCTTGAAGGTTCTGGAGAAACGATTGCAGTGATGGAATACTGGC 17324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17101 CAAGGITCAATCIAIGATCHCCTCHCHGATGCCGAATTAAAAACAGCAAGTGTCGCAGIC 17042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16922 ACAGGTTCTTCAAAGATTACTGCTCCAGGAACAGCCAAGAATGTTCTTTCCATTGGCTCA 16863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsnHisIleAlaGln 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 ProGlnAlaAsnLeuValPheGlnSerIleMetAspSerSerGlyGlyLeuGlyGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AsnSerTrpGlyAlaProValAsn---GlyAlaTyrThrAlaAsnSerArgGlnValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 GluTyrValArgAsnAsnAsp---MetThrValLeuPheAlaAlaGly---AsnGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 ProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAlaGlyAlaArgIleHisThr
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                                                                                                                                                                                                                                                                                                                                                                                                                             13 AlaGlnAsnAsnTyrGlyLeuTyrGlyGlnGlyGlnValValAlaAaAapThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 LeuTyrAla---LeuGlyArgThrAsnAsnAlaAsnAspProAsn---GlyHisGlyThr
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166
76
157
157
17
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Conservative:
Mismatches:
Indels:
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36.56%
27.09%
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                     364 ValaspaspieuaspieuValileThralaProasnGlyGlnLysTyrValGlyAspasp 383
                                                                                                                                                                           315 LeuAsnValAla------TyrValAsnGluAlaThrAlaLeu 326
                                                                                                                                                                                                                                   327 AlaThrGlyGlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIle 346
                                                                                                                                                                                                                                                                                             347 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSerTyrThr----------16u 363 :::||| |||:::||| |||||||
                                                                                                                                                                                                                                                                                                                                                                                                                   384 PheSerTyrProTyrAsp-----AsnAsnTrpAspGlyArgAsnAsnValGluAsn 400
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                                                                                                                296 GlyLeu---GlyTyrProSerGlyAspGlnGlyTrpGlyArgValThrLeuAspLysSer 314
257 ThrProlleValAlaGlyAsnValAlaGlnLeuArgGluHisPhelleLysAsnArgGly 276
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Alkali resistance; surface active agent resistance; detergency improver;
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                                                                                                                                                                                                                                                                                  Alkali-protease Ya enzyme gene.
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WPI; 1992-288440/35.
P-PSDB; AAR26274.
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Bacillus
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AAQ27516
 Aaq27516 Alkali-pr
Aav82382 Bacillus
Aax37277 Bacillus
Aax37279 Bacillus
Aax86667 Thermococ
Aax65926 WO9856926
Aax65926 WPPerther
                                       3, 2004, 16:37:54 ; Search time 335.908 Seconds (without alignments) 5476.111 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1201 GTATTTATAAAGGCTCCGCAATCTGGAACGTATATAATTGAGGTTCAAGCGTATAATGTA 1260
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                                AsnGlualaThralaLeualaThrGlyGlnLysAlaThrTyrSerPheGlnAlaGlnAla
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flavour; ss.
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                                                     The sequence is that of the alkali-protease Ya enzyme gene which can be used in the recombinant production of Ya enzyme. Ya enzyme is excellent in alkali resistance and surface active agent resistance and improves detergency
                                                                                                                                                                                                                                                                                                                 ValGiyAlaThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsnHis
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DNA coding alkali-protease Ya enzyme - has good alkali and surfactant resistance and improves detergency.
                                                                                                                                            Sequence 1299 BP; 401 A; 246 C; 297 G; 355 T; 0 U; 0 Other;
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Conservative:
Mismatches:
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                                        Claim 3; Page 2; 17pp; Japanese.
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P-PSDB, AAW89547.

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Novel protease from Bacillus subtilis LC20 - useful in laundry and dishwashing detergents and for leather processing.

PT dishwashing detergents and for leather processing.

RS

Claim 11; Page 52-53; 77pp; English.

CC

CC

CC

Contained in Bacillus subtilis LC20 NRKL B-21680. The protease gene was contained in Bacillus subtilis LC20 NRKL B-21680. The protease gene was contained in Bacillus subtilis LC20 NRKL B-21680. The protease gene was contained in Bacillus subtilis LC20 NRKL B-21680. The protease gene was contained in Bacillus subtilis LC20 NRKL B-21680. The protease gene was contained in Bacillus subtilis LC20 NRKL B-21680. The protease gene was contained in method for producing the protease. The gene by inverse PCR (see AAV82410-11), reconstruction of 65' and 3' ends and contained and dishwashing detergents, for institutional and industrial cannot dishwashing detergents, for institutional and industrial cannoting the degree of hydrolysis of proteins, degradation of undesired containing the degree of hydrolysis of proteins, degradation of undesired containing the provades mutant containing the provades mutant containing the protease activity is diminished. Such cells mutant containing the protease activity is diminished. Such cells can be used in which the protease activity is diminished. Such cells can be used for the production of heterologous recombinant proteins

XX

Sequence 3003 BP; 982 A; 504 C; 645 G; 972 T; 0 U; 0 Other;
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US-09-985-689A-5 (1-433) x AAV82382 (1-3003)

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qq	1470 2	AATGACGTGGCCCGTGGCATTGTGAAGCAGACGTCGCACAAAATAACTTTGGCTTATAT 1520	59
č	21	GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArgAsnAspSer 40	
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Dp	1590 7	TCGATGCATGAAGCATTCCGCGGTAAGATTACCGCACTATATGCACTGGGCAGAACGAAT 164	49
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Db	1650 7	AACGCCAATGATCCAAATGGACATGGAACCCATGTTGCTGGATCTGTGTTAGGAAATGCT 1709	60
ζò	81 1	LeuasnLysGlyMetalaProGlnalaAsnLeuValPheGlnSerIleMetAspSerSer 100	0
Db	1710 /	ACAAATAAAGGGATGGCACCGCAAGCCAATCTAGTCTTTCAATCTATTATGGATAGTGGT 1769	69
ζ	101	GlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAla 120	0
Db	1770 (	3CT 182	129
à	121 (	14	0
QQ	1830	GARGCGAGAATTCATACGAATTCATGGGGGCTCCAGTAAACGGTGCCTATACGACAGAC 188	60
٥٨	141	SerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGly 160	0
QQ	1890	TCTCGAAATGTTGATGATTATGTGAGAAAAAAGATATGACGATTCTTTTTGCGGCCGGA 194	949
٥٨	161	AsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsnAla1leThr 180	0.
QQ	1950	AATGAGGGACCAGGTAGGGGTACAATCAGTGCACCAGGAACAGGAAAAAAAA	600

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                                                          070 gridereaarreneredaggreeracracaagargaacgridaraaggeggacgacgacarg
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                                                                                                                         241 AlaasnTyrasnSerLygTyrAlaTyrMetGlyGlyThrSerMetAlaThrProlleVal
ValGlyAlaThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsnHis
                                                                                AlaProGlyThrPhelleLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrp
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                                GlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIle
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Nomura M;
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P-PSDB; AAY17091.
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The invention relates to alkaline proteases produced by strains of Bacillus. The proteases ability to digest casein is not inhibited by oleic acid and they have a high stability to oxidising agents. The alkaline protease of the invention has the following properties: (a) it is active over the pH range 4-13 and has at least 80% of its optimum activity over the pH range 6-11; (b) after 30 minutes at 40 deg. C it is stable over the pH range 6-11; c) its isoelectric point is 8:9-9.1; (d) its ability to digest casein is not inhibited by oleic acid; (e) it has molecular weight about 43,000 by SDS-PAGE. The alkaline proteases can be used as enzymes in washing compositions for use in automatic dishwashers and for washing clothes. The stability to oxidising agents allows the benzyme to be an effective component of washing compositions including bleaches. The present squence represents an alkaline protease encoding DNA. (Updated on 20-MAR-2003 to correct DR field.)
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             digestion; oleic acid;
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             protease; Bacillus; casein di
composition; oxidising agent;
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                                                     SerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGly
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715 GGAAGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the coding sequence for the protease from Thermococcus celer DSM-2476. This sequence encodes a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, drug and chemical industries. (Updated on 17-OCT-2003 to standardise OS field)
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Gecaaggicataggciggtaggcggcgigacgaggigaccag
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                                                                                                research reagent; thermal stability; thermococcus celer;
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                                                                    Thermococcus protease coding sequence.
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                                                                                                                                Thermococcus celer; DSM-2476
                                                                                                                                                                                                                                                                                     (TAKI ) TAKARA SHUZO CO LTD
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                       (revised)
(first entry)
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Best Local Similarity:
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Tsunasawa S,
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Pred. No.:
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The invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40-110 deg.C (optimum 80-95 deg.C), working ph 5-10 (optimum 6-8), and retains more than 90% of its activity after 8 hours at 95 deg.C. The invention also provides gene sequences encoding a polypeptide of formula 81G-Aha-61y-61y-Asn-PRO, where 81G is a signal peptide from subtilisin, and PRO is the work protease. Host cells (especially Bacillus strains) transformed with vectors comprising the genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and for chemical synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant hyperthermostable protease from Pyrococcus furiosus - and gene encoding it, for large scale production of the protease for
                                                                                                           Hyperthermostable, protease, thermophilic, bacterium, subtilisin, additive; drug, washing agent, foodstuff; chemical synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1977 BP; 453 A; 659 C; 554 G; 311 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                    Takakura H, Morishita M, Shimojo T, Asada K, Kato I;
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                                                                                                                                                                                                                                                                                     97JP-00151969.
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                                              06-MAY-1999 (first entry)
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Pred. No.:
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8 ValLysalaaspvalalaGlnasnAsnTyrqlyLeuTyrGlyGlnGlyGlnValValAla 27
                                                                                        28 ValAlaAspThrGlyLeuAspThrGlyArgAsnAspSerSerMetHisGluAlaPheArg 47
                                                                                                                                                                                 GlyLysileThrAlaLeuTyr---AlaLeuGlyArgThrAsnAsnAlaAsnAspProAsn 66
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LeMet :::::	uPheser : CGTCCAG	lAsnGly.	tThrval: AGTAGTC	YThrAla     cgccGcG	rLeuAla GTT	VArgile     :::	uAlaProAs	rSerMet          CAGCATG	BASDArg ::: CCACCCG	lealagiyalath 	ThrLeu   GAACGTC	ygln crccgrc	roLeuLysIleSe ::: rcGTGACCGCCAC	1Asnasp 	eSerTyr     TGACTAC	nalabro       	oGlnArg
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-i [ )	oSerAsnLeuAsnThrLe ::: ::::: CGCGGGTGTTGACTGGGT	TrpGlyA    : :crcGGCT	Argasna ::: TGGGACG	ileserA :::: GrcGGCT	Selection   Sele	AlaThrA      ccgacco	ProGlyThrPhelleLeuSerAlaArgs         CCCGGCGTTGACATCATAGCCCCGCGCG	TyrMetG PAGGCCT	ArgGluHisF	lebysAlaAlal   :::  CGAGACCGCC	1G1 yTrpG 	ralaLeu2 3CTCACCT	hlaglyI Iggcgccz	SerTyr1	ProAsnGlyGlnLysTyrValGlyAsnAspPheSerTy         CCCAACGGGAACGAGGTTGACTA	Asnvale       	ThrileGluvalGlnalaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaile
roginalaasnieuva 	suProser	rAsnser     	luTyrva] ACAACGC	erGlyTha ::      CTACACC	snTyrArg	erArgGl)          scAGGGG	leLeuse   :::::  CATAGC	aasntyrasnserlystyralatyrmet 	JLeu HATC	rLeulleLys::      :::	lyAspGlı	lualath:     acgccaac	lnAlaglı ACGTCAG	hrThrAle	lnLysTy	snvalglı    GCTTCGA(	laTyrAsı ::    GCTAC
AlaProG	uglyglyter:::: ::: CTCCACCAT	IlenisT) ::: GTCATCA	valaspG. GCCGTCA	ProAsnS       : CCGAACA	ThrGlua	Phesers        TTCTCCA	ThrPhel GTTGACA	AsnSerb     AACGACT	Ala CGCG	Prosert  :::  Accecc	ProserG	ValAsnG	serPheG	GlySerT	AsnGlyG      AAC	ArgAsnA G	valgina            Greerea
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83 LY 655 AT	101 GI    715 GG	121 Gl 	141 Se 835 CT	161 As    895 AA	181 Va    955 GT	201 II    982 AT	221 Ale	241 Ald	261 Al :: 1153 TC	280 1204 AAG	297 Le :: 1264 AT	317 Va :: 1303 AT	332 Ala 	352 AB	7.2	392 Tr :: 1498 TA	412 Th

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AAT-----AGCGACCTTGATCACTCTACGAT 1062
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                                                                                                                                                                                                                                                                                                                                                                                 AlaThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsnHisIleAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant hyperthermostable protease from Pyrococcus furiosus gene encoding it, for large scale production of the protease for
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                                                    GluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
                                                                                                                                                                                                                   reagent; thermal stability; pyrococcus furiosus;
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                     ---ACC 1095
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                                                         GlyArgAsnAsnValGluAsnValPhelleAsnAlaProGlnSerGlyThrTyrThrIle 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the coding sequence for the protease from Pyrococcus furiosus DSM-3638. This sequence encodes a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can be used as research reagents, and industrially in the food, dury and chemical industrials. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                research reagent; thermal stability; pyrococcus furiosus; ss.
                                                                                                                                     GluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
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Matches:
Conservative:
Mismatches:
CCCAATGGAAACCAGGTT-----GACTACTCTTAC
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(first entry)
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P-PSDB; AAW24129.
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Best Local Similarity:
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Tsunasawa S,
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20-APR-1998
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GlyArgAsnAspSerSerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAla

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The invention relates to a hyperthermostable protease derived from a thermophilic bacterium (especially Pyrococcus furiosus). The protease has working temperature 40-110 deg.C (optimum 60-95 deg.C), working ph 5-10 (optimum 6-8), and retains more than 90% of its activity after 8 hours at 95 deg.C. The invention also provides gene sequences encoding a polypeptide of formula SIG-Ala-Gly-Gly-Asn-PRO, where SIG is a signal peptide from subtilisin, and PRO is than above protease. Host cells (especially Bacillus strains) transformed with vectors comprising the genes are used for the recombinant production of the protease. The hyperthermostable protease which can be prepared in quantity suitable for industrial use, can be used as an additive for drugs, washing agents and foodstuffs and for chemical synthesis
                                1492 GCCTACTATGGATTCGAAAAGGTTGGTTATTACAACCCAACTGATGGAACATGGACAATT 1551
                                                                                                    1552 AAGGITGIAAGCIAC-----AGCGGAAGTGCAAACTATCAAGTAGATGTGGTA 1599
                                                                    GluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
GlyArgAsnAsnValGluAsnValPhelleAsnAlaProGlnSerGlyThrThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - and
                                                                                                                                                                                                                                                                                                                  Hyperthermostable, protease, thermophilic, bacterium, subtilisin; additive, drug; washing agent, foodstuff; chemical synthesis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant hyperthermostable protease from Pyrococcus furiosus gene encoding it, for large scale production of the protease for industrial use.
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                                                                                            GluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
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---ATAGGATGGAAAGACTTTATCAACAACAAA 585
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  This sequence represents the DNA encoding the Thermoanaerobacter yonseii subtilisin-like serine protease of the invention. (Updated on 11-SEP-2003 to standardise OS field)
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ATAGCAATTATTGACACAGGTATAGACGGAAATCACGTTGACCTCTCA-------
                                        GluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432
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                              ArgThrAsnAsnAlaAsnAspProAsnGlyHisGlyThrHisValAlaGlySerValLeu
                                                          gecaccecacacacacadaaagaraaaacaacaacaacaacaacaacaacaaca
                                                                                            GlyAsnAlaLeuAsn------LysGlyMetAlaProGlnAlaAsnLeuVal
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                                                                                                                                                                                                                                                     1268 CTCGCCGGCATGGAGTGGGCGGCGCAGGGCGCCGACGTCGTCAACATGAGCCTGGGC
                                                                                                                                                                                                                                                                                                          144 ValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGlyAsnGluGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asymmetric hydrolase gene derived from Streptomyces viridosporus - acts on 4-substituted-1,4-di:hydro:pyridine derivatives to produce chiral derivatives useful for synthesis of cardiovascular drugs.
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                                                                                                                                                                       asymmetric hydrolase; dhpA; 4-substituted-1,4-dihydropyridine;
derivative; Streptomyces viridosporus; ester; chiral; synthesis;
cardiovascular; treatment; hypertension; ischaemic heart disease; ds.
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                                                                                                                                          Streptomyces viridosporus dhpA gene
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338. .2539
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                                              ВB
                                              AAT61454 standard; DNA; 2539
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96JP-00067478
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Yoshioka T;
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29-FEB-1996;
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Isshiki K,
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of e.g. hypertension and ischaemic heart disease. (Updated to standardise OS field)
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                                                                                  --AsnAsnValGlu 399
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                                                                  AsnValPhelleAsnAlaProGlnSerGlyThrTyrThrIle-------
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338. .2809
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2540. .2809
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/product="Welanin"
/product="Melanin"
/product="from S. antibioticus"
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                 SerTyrProTyrAspAsnAsnTrpAspGlyArg
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Isshiki K, Yoshioka T;
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29-FEB-1996;
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1958 ACGTCGACCGCCACCGAAGGCAAGGCGCCCCCGGGGGTTCTTCACGCTGGGC 2017
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                                                                              320 ValAsnGluAlaThrAlaLeuAlaThrGly-----329
                                                                                                                               330 ------GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProjeuLysIle 346
                                                                                                                                                                                    347 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal 364
                                                                                                                                                                                                                                       365 AsnAspLeuAspLeuValIleThrAlaProAsnGlyGlnLysTyrValGlyAsnAspPhe 384
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Sequence 12, Appli
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US-00-873-479-41

Sequence 41, Application US/08873479

Sequence 41, Application US/08873479

Patent No. 5891701

APPLICANT: Sloma, Alan

APPLICANT: Lynne, Christianson

TITLE OF INVENTION: Having Protease Activity

TITLE OF INVENTION: Having Protease Activity

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 58917010 No. 5891701t
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CITY: New York
CITY: New York
CITY: New York
COMPUTRY: USA
ZIF: 10174
COMPUTRY: BADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTR: IBM Compatible
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MEDIUM TYPE: Diskette
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MADITALION NUMBER: US/08/873,479
FILING DATE: UNW-1997
CLASSIFICATION NUMBER: 34,086
REPRENCE/DOCKET NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELECOMMUNICATION:
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TELECOMU
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US-08-18-173-172
US-09-514-340-3

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US-08-750-532-2

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US-08-894-818B-7

US-09-445-25

US-08-894-818B-15

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          **MODEL=frame+ pzn.model - DEV=Xlh
-Q=/Cgn2 1/USPTO_spool/US09985689/runat_31032004_161807_4184/app_query.fasta_1.3498
-Q=/Cgn2 1/USPTO_spool/US09985689/runat_31032004_161807_4184/app_query.fasta_1.3498
-DB=Issued Patents NA -QFFN=fastap -SUFFIX=ni -MINNATCH=0.1 -LOOPECL=0
-LOOPEXT=0 - UNITS=Blts -START=1 - END=-1 - HATRIX=blosued 2 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODE-LOCAL - OUTFMT=pto - NOFM=ext - HEAPSIZE=500 - MINIEN=0 - MXLEN=200000000
-USBREAUS09985699_GCGN 1 1 1.44 @ erunat_31032004 161807 4184 - NCPU=6 - ICPU=3
-NO MMAP - LARGEQUERY - NEG SCORES=0 - WAIT - DSPENCCK=100 - LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 3, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 11, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 6, Appli
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                                                                                                                                                                                                                                      April 3, 2004, 23:50:44; Search time 63.4512 Seconds (without alignments) 3787.066 Million cell updates/sec
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1 NDVARGIVKADVAQNNYGLY......BVQAYNVPSGPQRFSLAIVH 433
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11. /GGN2_6/ptodata/2/ina/5A_COMB.seq:*
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17. /GGN2_6/ptodata/2/ina/PGTUG_COMB.seq:*
17. /GGN2_6/ptodata/2/ina/PGTUG_COMB.seq:*
                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                           nucleic search, using frame_plus_p2n model
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US-09-445-472-2
US-08-894-818B-4
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                                                       301 SerGlyAspGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAlaTyrVal
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Sequence 3, Application US/09509814A

Patent No. 637627

GENERAL INFORMATION:
APPLICANT: TAKAIWA, MIKIO
APPLICANT: SARKI, KATSUHISA
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KUBOTA, HIROMI
APPLICANT: KAGEYANA, YSAUSHI
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APPLICANTON NUMBER: US/09/509,814A
CURRENT FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08

PRIOR FILING DATE: 1997-06-08

NUMBER OF SEQ ID NOS: 24

SECTWARE: PATENT IN VERSION 3.0

SEQ ID NOS: 24

SECTWARE: PATENT IN VERSION 3.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                      1.63e-194
2044.00
94.69%
89.15%
90.40%
                                                  TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
              base pairs
                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                                                                                US-08-873-479-41
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JOS-09-509-104-0.

JOSCHOLOS T. Application US/09509814A

PACHOLOSATION:

APPLICANT: TAKAINA, MITSUYOSHI

APPLICANT: SAEKI, KATSUHISA

APPLICANT: SAEKI, KATSUHISA

APPLICANT: HITOMI, JUN

APPLICANT: HITOMI, JUN

APPLICANT: HITOMI, JUN

APPLICANT: SHIKAINA, MASAFUMI

TITLE OF INVENTION: ALKAINE PROTEASE

FILE REPERENCE: 0327-0932-0-CT

CURRENT APPLICATION NUMBER: US/09/509,814A

CURRENT FILING DATE: 1998-10-07

PRIOR FILING DATE: 1998-10-07

PRIOR FILING DATE: 1998-10-07

PRIOR FILING DATE: 1998-06-08

NUMBER OF SEQ ID NOS: 24

SEQUENCE: PARCHELING PARCHELON SEQUENCE: SECONDATE: 10-07

PRIOR FILING DATE: 1997-06-08

NUMBER OF SEQ ID NOS: 24

SEQUENCE: APPLICATION VERSION 3:0

SEQUENCE: APPLICATION VERSION 3:0
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94.24%
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88.43%
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ORGANISM: Bacillus sp.
FEATURE:
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                                 AATGATGTGGCCAGAGGTATTGTCAAAGGGGATGTGGCACAGAGCAGCTACGTTGTAT 675
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                                                 GENERAL INFORMATION:
APPLICANT: OKUDA, MIKICO
APPLICANT: OKUDA, MIKIGONICANI: SAEKI, KATSUHISA
APPLICANT: SAEKI, KATSUHISA
APPLICANT: KUBOTA, HIRONI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: KAGEYAMA, YASUSHI
APPLICANT: SHIKATA, SHIKGUM
APPLICANT: SHIKATA, SHIKGUM
APPLICANT: NOMURA, MASAFUMI
APPLICANT: NOMURA, MASAFUMI
APPLICANT: NOMURA, MASAFUMI
APPLICANT: NOMURA, NOMURER: 105/09/509,814A
CURRENT APPLICATION NUMBER: PCT/UP98/04528
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN VERSION 3.0
SENGTHAN: 1923
     Sequence 5, Application US/09509814A, Patent No. 6376227, GENERAL INFORMATION:
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1998.50
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87.79%
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Best Local Similarity:
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US-09-509-814A-5
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                                                           SerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsn 119
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             1639 GCCGGCAGCCTTTGAAAACTCCCTGGTATGGTCTGATGCCCCTGCGAGGCCAAACTGCT
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                                                                                 AsnSerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAla
AlaLeuAsniysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSer
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAKAKURA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
LENGTH: 1977 base pairs
                                         D.C.
: United States of America
419 Seventh Street N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic DNA
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46.03%
31.07%
19.59%
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STRANDEDNESS: double
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    CITY: Washington STATE: D C
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Best Local Similarity:
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                                                               COUNTRY:
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                                                        ACAGTCGGAGCTACGGAAAACCTCCGCCCAAGCTTTTGGGTCTTATGCGGACAATATCAAC 1218
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                        GlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIle 179
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APPLICANT: TAXAKURA, Hikaru
APPLICANT: TAXAKURA, Hikaru
APPLICANT: MORISHITA, Mao
APPLICANT: MITTA, Masanori
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
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GlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAla 120 GGAAGCGICTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTAC 774 ||||||||:: | GGCAAGGTCATAGGCTGGTACGACGGCGTCAACGGCAGGTCGACCCCCTACGATGACCAG 594 28 ValalaAspThrGlyLeuAspThrGlyArgAsnAspSerSerMetHisGluAlaPheArg 47 glyнisglyThrHisValAlaGlySerValLeuGly------АвлАlаLeuAвл LysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMet-----AspSerSer 655 ATAGGCGTCGCCCCCGGCGCGAAGCTCGTCGGCGTCAAGGTTCTCGGTGCCGACGGTTCG GlyAlaArg11eHisThrAsnSerTrpGlyAlaProvalAsnGlyAlaTyrThrAlaAsn GlyLysileThrAlaLeuTyr---AlaLeuGlyArgThrAsnAsnAlaAsnAspProAsn 8 VallysalaaspValalaGlnasnAsnTyrGlyLeuTyrGlyGlnGlyGlnValValAla 1977 137 66 170 68 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: ELONGY disk
COMFUTER: ELONGY disk
COMFUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FLING DATE: 20-MAY-1998
CLASSIFICATION NUMBER: PCT/UP96/03253
APPLICATION NUMBER: PCT/UP96/03253
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/UP96/03253
FLING DATE: 07-NOV-1996
FRICH APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION: Length: Matches: Conservative: Mismatches: Indels: US-09-985-689A-5 (1-433) x US-08-894-818B-2 (1-1977)

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Percent Similarity:
Best Local Similarity:
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                                                     ilealaGlnPheSerSerArgGlyAlaThrArgAspGlyArgIleLysProAspValThr
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                 crcagrcádecegreaacaacecerdegaceceggraragradiérecercécédede
                                       AsnGluGlyProAsnSerGlyThrlleSerAlaProGlyThrAlaLysAsnAlaileThr
                                                                                                                                                                                                          241 AlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrSerMetAlaThrProlleVal
141 SerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGly
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Patent No. 6358726
GENERAL INFORMATION:
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US-09-445-472-11
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APPLICANT: TAKAKURA, Hikaru APPLICANT: MORISHITA, Mio APPLICANT: SHIMOJO, Tomoko

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APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERENCE: PACAKURA=6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 11
LENGTH: 1977
                                                                                                                                                                                                                                                                                                         1977
137
66
170
68
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic
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443.00
46.03%
31.07%
19.59%
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Alignment Scores:  Pred. No.:  Pred. No.:  422.50  Matches:  138  Score:  Percent Similarity:  13.64  Conservative: 55  Best Local Similarity:  18.69  Mismatches:  167  Query Match:  4.69  18.69  Gaps:  17  US-09-985-689A-5 (1-433) x US-09-445-472-2 (1-1236)  Qy  16 AsnTyrGlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThr 35  17  Db  58 AACTTGGAATAGATGGTTCTGGAATCACAATAGGAATAATTGACACTGGAATTGAC 114  Dv  36 GlvArgAsnAspSerSerMetHisGluAlaPheArGGlyLyslleThrAlaLeuTyrAla 55						GlyalathrarghspclyargilelysProAs	7 17	alalagly 26	Qy 263 AgnValAlaGlnLeuArgGluHisPhelleLy8A8nArgGlylleThrPro 279	Qy 280 LysProSerLeulleLysAlaAlaLeulleAlaGlyAlaThrAspValGlyLeuGly 298	Cy 299 TyrProSerGlyAspGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAla 318
	Qy         297 LeuGlyTyrProSerGlyAspGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsn 316           Db         1264 ATCGCCTAC	Qy 332 AlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIleSerLeuValTrpThr 351	372 ThralaproAsnGlyGlnLysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsn 372 ThralaproAsnGlyGlnLysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsn 1453 TACGACCCCAACGGGAACGAGGTTGACTACTCCTACCTAC 392 TrpAspGlyArgAsnAsnValGluAsnValPheIleAsnAlaproGlnSerGlyThrTyr	Db 1498 TACGGCTTCGAGAAGGTCGGCTACTACAACCCGACCGGAACCTGG 1545  Qy 412 ThrileGluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIle 431        ::::::      :::::      ::::::      ::::::	Cy 432 Val 432 	US-09-445-472-2 Sequence 2, Application US/09445472 Fatent No. 6358726 GENERAL INFORMATION: APPLICANT: TAKAKURA, Hikaru	APPLICANT: MORISHITA, Mio ; APPLICANT: SHIMOJO, TOMOKO ; APPLICANT: ASADA, Kiyozo ; APPLICANT: KATO, Ikunoshin	; TITLE OF INVENTION: SYSTEM FOR BAFRFESSING HIFERINGSADES ; FULR REFERENCE: TAKANGRA-6 ; CURRENT APPLICATION NUMBER: US/09/445,472 ; CURRENT FILING DATE: 1999-12-06	FALOR FILING DATE: 1997-06-10; NUMBER OF SEQ ID NOS: 33; SOFTWARE: PatentIn version 3.0	; SEQ ID NO 2 ; LENGTH: 1236 ; TYPE: DNA ; ORGANISM: Artificial Sequence	; FBATURE: ; OTHER INFORMATION: Synthetic US-09-445-472-2

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                                                  OTHER INFORMATION: /note= N at position 1283 is G or
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167
179
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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            MOLECULE TYPE: genomic DNA FEATURE:
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422.50
43.96%
31.44%
linear
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1033 AAT-----AGCGACCTTGATCTTTACCTCTACGAT 1062
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                                                                                                                                                               319 TyrvalAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAla------Thr 333
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APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUMASAWA, Susumu
APPLICANT: TSUMASAWA, Susumu
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
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ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: ISM PC compatible
COMPUTER: BM PC compatible
SUSTMARE: PATENTIN Release #1.0, Version #1.30
EVERSENT APPLICATION DATA:
FLING DATE: 20-MRY-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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419 Seventh Street N.W., Ste. 300
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FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
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: United States of America
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; Sequence 34, Application US/08B94818B
; Patent No. 6261822
; GENERAL INFORMATION:
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REGISTRATION NUMBER: 25,618
REPERENCE/DOCKET NUMBER: TAI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
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ADDRESSEE: Browdy and
STREET: 419 Seventh &
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 LeuGlyArgThrAsnAsnAlaAsn------AspProAsnGlyHisGly 69
                                                                                                                                                                                                                                                                                                                                                                                               16 AgnTyrGlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAgpThrGlyLeuAgpThr 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 GlyArgAsnAspSerSerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAla 55
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                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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TELBFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1962 base pairs
                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECTLE TYPE: genomic DNA
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43.96%
31.44%
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Best Local Similarity:
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CCCAATGGAAACCAGGTT-----ACTACTCTTAC------ACC 1491
                                                                  AAAACAGCCCTCATAGAAACTGCTGATATCGTAAAGCCAGATGAAATAGCCGATATAGCC 1269
                                                                                                                                                                                                                                                                                                                                                                                                    1492 GCCTACTATGGATTCGÁAAAGGTTGGTTATTACAACCCAACTGATGGAACATGGACAATT 1551
                                                                                               TyrProSerGlyAspGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAla 318
                                                                                                                                                    TyrValAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAla-----Thr 333
                                      LysProSerLeulleLysAlaAlaLeulleAlaGlyAlaThrAspValGly---LeuGly 298
                                                                                                                                                                                                        334 TyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIleSerLeuValTrpThrAspAla 353
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                                                                                                                                                                                                                                                                                                                                                                        394 GlyArgAsnAsnValGluAsnValPheIleAsnAlaProGlnSerGlyThrTyrThrIle 413
                                                                                                                                                                                                                                                                                                                    ProAsnGlyGlnLysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsnTrpAsp 393
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APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: HIMOOO, Tomoko
APPLICANT: KATO, Ikuosehin
ITLE OF INVENTICM: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
CURRENT APPLICATION UNDER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR PELING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
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Mismatches:
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Matches:
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Patent No. 6358726
GENERAL INFORMATION:
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422.50
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Best Local Similarity:
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LENGTH: 1962
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988 AGCTTCTCAAGCAGAGGGCCAACTGCAGACGGCTTAAGCCTGAGGTTGTTGCTCCA 1047
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454 AACTTGGGATATGATGGTTCTGGAATCACAATAGGAATAATTGACACTGGAATTGAC--- 510
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16 AsnTyrGlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThr 35

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1159 GTTGGCGCTCATCCTCCAG------GCCCACCCGAGCTGGACCCCGGACAAGGTG 1209
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                                                                                                           56 LeuGlyArgThrAsnAsnAlaAsn ------AspProAsnGlyHisGly
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                    16 AsnTyrGlyLeuTyrGlyGlnGlyGlnValValAlaNalAlaAspThrGlyLeuAspThr
                                   36 GlyArgAsnAspSerSerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAla
                                                                            ThrisvalalaglySerValLeuGly------AspAlaLeuAsnLysGly
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MOLECULE TYPE: genomic DNA
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Percent Similarity: 41.28% Conservative: 53 Best Local Similarity: 29.58% Mismatches: 168 Query Match: 15.50% Indexs: 98 DB: 3 Gaps: 19	US-09-985-689A-5 (1-433) x US-09-000-016-3 (1-2539)	nGlyGlnValValAlaValAlaAspThrGly	AGGCGTGA	nrAlaLeuTyrAlaLeuGly 57	Db 1055CATCCGGACCTGAAGGCCGGGTGACGCGCTCAAGAACTTCACC 1099	sGlyThrHisValAlaGlySerValLeu 77	GATCGCGGCG 1	78 GlyAsnAlaLeuAsnLysGlyMetAla	CCCGGCGCGCGAICCIC 777	Qy 93 PheGlnSerIleMetAspSerSerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThr 112 RIV	1220 AACGGCAAGGTCCTCGACGATCCC		-	1328 GGCATGGACACACGGAGACCGACGCTGAAGCGGGGG	144 ValAs	   1367 GTCGA	64 ProAsnSerGlyThr	2252		1481	15	Qy 223 GlyThrPheIleLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsn 242	ceccrcee	313	cesciacarcarcrecededacercearecedecedes		AGCAGCAGCACCCCGAC	3lyLeuGlyTyr [	GCGGCAAGTAC	ThrLeuAspLysSerLeuAsnValAlaTyr 3	TCCAGCAGACCGTG	Oy 320 ValAsnGiuAlaThrAlaLeuAlaThrGly329
Qy 354 ProGlySerThrThrAlaSerTyrThrLeuValAsnAspLeuAspLeuVallleThrAla 373	374 ProAsnGlyGlnLysTyrValGl		TYTHTYT	Db 1501GGCTTCGAGAAGGTCGGCTACTACAACCCGACCGGAACCTGGACGGGGGGGCTC 1551	Qy 414 GluValGlnAlaTyrAsnValProSerGlyProGlnArgPheSerLeuAlaIleVal 432		REGULT 12	US-09-000-016-3 ; Sequence 3, Application US/0900016 ; Patent No. 6143541	GENERAL INFORMATION:	APPLICANT AKITE AKISHMA EL AL. TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERI	; TITLE OF INVENTION: ITS EXPRESSION PRODUCT ; NUMBER OF SEQUENCES: 7	CORRESPONDENCE ADDRESS:   ADDRESSE: Wanderorth Lind & Ponack, L.L.P.	Washington	; STATE: D.C. ; COUNTEY: U.S.A. ; ZIP: 20006	齿毛	ible -DOS	8 2	; APPLICATION NUMBER: US/09/000,016 ; FILING DATE: January 30, 1998	; CLASSIFICATION: 530 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER:	; FILING DATE: ; ATTORNEY/AGENT INFORMATION:	NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 PEREPRENCE/JOCKET NUMBER:	TELECOMMUNICATION INFORMATION: TELEPHONE: 202-721-8200	; TELEFAX: 202-721-8250 ; TELEX:	; INFORMATION FOR SEQ ID NO: 3: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 2539 base pairs ; TYPE: nucleic acid	; STRANDEDNESS: double ; TOPOLOGY: linear	omic D	; ORGANISM: Streptomyces viridosporus ; STRAIN: A-914	CDS	ON: FICAL	5-200-000-50-50-50-50-50-50-50-50-50-50-50-	Alignment Scores: 3.7e-25 Length: 2539 Pred. No.: 350.50 Matches: 134

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Patent No. 6361987
GENERAL INFORMATION:
GENERAL INFORMATION: GENE ARISAWA et al.
APPLICANT: Akira ARISAWA et al.
TITLE OF INVENTION: GENE MYDOLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE
ITS EXPRESSION PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2047
                                                                                                                                                                                         899 CCGGTCACCAGCAGCTGACCTACCGCAACCTCGGCACCCAGGACGTCACGCTGAAGCTG 1957
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1838 ATCGCCGACCCGGTCTCGGTGAGCTTCGGCGTCCAGCAGTGGCCGCACACCGACGACGAG 1897
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                                                                                                                                                                                                                                                                                                                              SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Streptomyces viridosporus
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REGIGINATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: «Unknown>
TELECOMMUNICATION INFORMATION:
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RAPLICATION NUMBER: US/09/514,340
FILING DATE: 28-Feb-2000
CLASSIFICATION: vUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION WUMBER: 09/000,016
FILING DATE: January 30, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
ADDRESSE: Wenderoth, Lind &
STREET: 2033 K Street, N.W.,
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MEDIUM TYPE: Diskette, 3.5
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
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SEQUENCE CHARACTERISTICS:
LENGTH: 2539 base pairs
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STRANDEDNESS: double
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COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGlyAsnGluGly
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133
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                     ORGANISM: Streptomyces antibioticus STRAIN:
                                                                                                                                     Streptomyces viridosporus
                               LENGTH: 2809 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
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345.50
41.068
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US-09-000-016-1
                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 338...2539
IDENTIFICATION METHOD:
                  SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
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Best Local Similarity:
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STRAIN: A
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Sequence 1, Application US/09000016

Battent No. 6143541

GENERAL INFORMATION:
APPLICANT: Akira ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HYPROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV
TITLE OF INVENTION: HYPROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV
TITLE OF INVENTION: HYPROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV
TITLE OF INVENTION: HYPROLASE ACTIVITY & RESERVENT OF A STREET: 2013 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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838 ATGGCCGACCCGGTCTCGGTGAGCTTCGGCGTCCAGCAGTGGCCGCACACCGACGACGAG 1897
                                                                    ProSerGlyAspGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAlaTyr 319
                                                                                                                                                                                                            -----GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIle 346
                                                                                                                                                                                                                                                                                                                                                   365 AsnAspLeuAspLeuVallleThrAlaProAsnGlyGlnLysTyrValGlyAsnAspPhe 384
                                                                                                                                                                                                                                                                                                                                                                                                                        ----AsnAsnValGlu 399
                                                                                                                                                                                                                                                                               347 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal 364
                                                                                                                                       320 ValAsnGluAlaThrAlaLeuAlaThrGly------
     ---IleAlaGlyAlaThrAspValGlyLeuGlyTyr
                                                                                                      1778 Accecentegageageagenregageegarceaggeegacaacaacaacaacageegregae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GluValGlnAlaTyrAsnVal-ProSerGly 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,016
FILING DATE: January 30, 1998
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NAME: Warren M. Cheek, Jr.
REGISTRATION UNDMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEFAK: 202-721-8250
       LeuIleLysAlaAlaLeu----
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---provalAsnGlyAlaTyrThrAlaAsnSerArgGln 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AsnAspSerSerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAlaLeuGly
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Matches:
Conservative:
Mismatches:
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STRAIN: <Unknown>
                                                                                                                                                                                                                                                                                                                                               <Unknown>
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,340
FILING DATE: 28-Feb-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                           PRIOR APPLICATION DATA:

RIPLING DATE: January 30, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Lee Cheng

REGISTRATION NUMBER: 40,949

REFERENCE/DOCKET NUMBER: 40,949

TELECOWTUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELERAX: 202-721-8250

TELERA: 202-721-8250
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NO: 1:
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IDENTIFICATION METHOD:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
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IDENTIFICATION METHOD
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Patent No. 6351987
GENERAL INFORMATION:
GENERAL INFORMATION: GENE ENCOING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: GENE ENCOING A PROTEIN HAVING ASYMMETRIC
ITLE OF INVENTION: GENE ENCOING A PROTEIN HAVING ASYMMETRIC
ITLE OF INVENTION: GENE ENCOING A PROTEIN HAVING ASYMMETRIC
ITLE OF INVENTION: GENE ENCOING A PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2047
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1898 CCGGTCACCAAGCAGCTGACCGCAACCTCGGCACCCAGGACGTCACGCTGAAGCTG 1957
                                                                                                                                                                                                                                                                                                ------CACCCCGAC 1720
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                                                             1508 TTCTCCACCGGCCCCGCCTCGGCGACGCGCCATCAAGCCGGACGTCACGCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 SerLeuValTrpThrAspAlaProGlySerThrThrAlaSer-----TyrThrLeuVal 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AsnAspLeuAspLeuValIleThrAlaProAsnGlyGlnLysTyrValGlyAsnAspPhe 384
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                                                                                                                      GlyThrPheileLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsn 242
                                                                                                                                                                                                                                                                                                                                                                                 263 AsnvalAlaGlnLeuArgGluHisPhelleLysAsnArgGlylleThrProLysProSer 282
PheSerSerArgGly---AlaThrArgAspGlyArglleLysProAspValThrAlaPro 222
                                                                                                                                                                                                                                                           243 TyrAsnSerLysTyrAlaTyrMetGlyGlyThrSerMetAlaThrProlleValAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 LeuilelysAlaAlaLeu------IleAlaGlyAlaThrAspValGlyLeuGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1688 GCGCCCCCCCCCGAAGCAGCAG------
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SECTION OF S
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Sequence 5689, Ap
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US-10-385-662-1
Sequence 1, Application US/10385662
Publication No: US2040002432A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, KAZUHIRO
APPLICANT: SATO, KAZUHIRO
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SAEKI, KATSUHIRA
APPLICANT: SOBRIFINA
APPLICANT: NOWINA, MASAFUMI
TITLE OF INVENTION: ALKAINE PICTER
FILE REFERENCE: 234938USO
CURRENT APPLICATION NUMBER: UP 2002-081428
PRIOR APPLICATION NUMBER: UP 2002-165987
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-10-18
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-LOOPCLE - LOOPEXT=0 -UNITS=bits -STRAT=1 - PEN=-1 - MATRIX=blosum62
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1. \cgn2_6\prodata/1\pubpna/USO7 PUBCOMB.seq:*
2. \cgn2_6\prodata/1\pubpna/PCO7 BW PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result

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TGGGCGAACCATGACAGTAATATGCATACATGGGTGGAACGTCCATGGCTACACCGATC 780
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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94.24%
87.79%
88.39%
     PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.1
LENGTH: 1305
                                                     TYPE: DNA

GRGANISM: Bacillus sp. KG

FRATURE:

NAME/KEY: CDS

GOGATION: (1)...(1305)

GOTHER INFORMATION:

US-10-385-662-1
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Sequence 11, Application US/10090624

Publication No. US2002132335A1

GENERAL INFORMATION:

APPLICANT: TARACURA, Hikaru

APPLICANT: MORISHITA, Mio

APPLICANT: SHIMOJO, Tomoko

APPLICANT: SHIMOJO, Tomoko

APPLICANT: ARTO, Ikunoshin

TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

TILE REFERENCE: TARAKURA-6

CURRENT FILING DATE: 2002-03-06

PRIOR FILING DATE: 1997-06-10

PRIOR FILING DATE: 1997-06-10

PRIOR FILING DATE: 1997-06-10

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.0

EBEGID NO 11

LENGHT 1977

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                                                                                                                                                                                                                                                                        141 SerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGly 160
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ATAGGGGCCGATACCGTCTGGAACTCCCTCGGCTACGACGGAAGCGGTGGTGGTTGCC 492
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                                                                                                                GlytysileThrAlaLeuTyr---AlaLeuGlyArgThrAsnAsnAlaAsnAspProAsn 66
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                      ValLysAlaAspValAlaGlnAsnAsnTyrGlyLeuTyrGlyGlnGlyGlnValValAla
US-09-985-689A-5 (1-433) x US-10-090-624-11 (1-1977)
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Sequence 2, Application US/10090624

Publication No. USZ0020132335A1

GENERAL INFORMATION:
Hikaru

APPLICANT: TAXAKURA, Hikaru

APPLICANT: MORISHITA, Mio

APPLICANT: SHIMONO, Tomoko

APPLICANT: SHIMONO, Tomoko

APPLICANT: KATO, Ikunoshin

TILE REFERENCE: TAKAKURA=6

CURRENT APPLICATION NUMBER: US/10/090,624

CURRENT APPLICATION NUMBER: 09/445,472

PRIOR APPLICATION NUMBER: 1997-12-06

PRIOR APPLICATION NUMBER: 1997-12-06

PRIOR FILING DATE: 1997-06-10

NUMBER: PARCHING DATE: 1997-06-10

NUMBER: PARCHING DATE: 1997-06-10

SOFTWARE: PACENTIN VERSION 3.0

SEQ ID NO 2

LENGHH: 1236 1236 138 55 167 79 Length:
Matches:
Conservative:
Mismatches:

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MetAlaProGlnAlaAsnLeuValPheGlnSerIleMet-----AspSerSerGlyGly 102
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                                                                               Sequence 15, Application US/10090624

Publication No. US20020132335A1

GENERAL INFORMATION:
APPLICANT: TARAKURA, Hikaru
APPLICANT: TARAKURA, Hikaru
APPLICANT: ASADA, Kiyozo
ITILE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT APPLICATION NUMBER: US/202-0366
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Version 3.0
SEQ ID NO 15
LENGTH: 1962
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Matches:
Conservative:
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OTHER INFORMATION: Synthetic
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Best Local Similarity:
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                                                                    TYPE: DNA
; ORGANISM: Streptomyces atroolivaceus
US-10-314-657-1
; SOFTWARE: PatentIn version 3.2; SEQ ID NO 1; LENGTH: 135638
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APPLICANT: CHENG, Yi-Qiang
APPLICANT: CHENG, Yi-Qiang
APPLICANT: TANG, Gong-Li
TITLE OF INVENTION: Synthases and Methods of Use
TITLE OF INVENTION: Synthases and Methods of Use
FILE REFERENCE: 054030-0021
CURRENT APPLICATION NUMBER: US/10/314,657
CURRENT APPLICATION NUMBER: PCT/US02/08937
PRIOR APPLICANTION NUMBER: PCT/US02/08937
PRIOR FILING DATE: 2002-03-25
PRIOR FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 214
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                                                                                                                                                                                                                                                                  GlyThrPheIleLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsn 242
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AlaThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsnHisIleAla
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|S52 AAGGTTGTAAGCTAC-
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                                                SerieullelysAlalaLeulleAlaGlyAlaThrAspValGlyLeuGlyTyrProSer 301
                                                                                                GlyAspGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAlaTyrValAsn 321
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Fatent No. US20020146721A1
GENERAL INPORMATION:
APPLICANT: Berka. Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: DATES STORESSION
FILE REFERENCE: 10085.500-US
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAMA, JUN
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1254 GCTGGCGTCCTTCTCCCAGCGCGCGGCCTGGACGGCGCCATCAAGCCCGACGTCAC 1313
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                                                                                                                                                                                                                                  257 rProllevalAlaGlyAsnValAlaGlnLeuArgGluHisPhelleLysAsnArgGlyIl
                                                          220 ralaproglyThrPhelleLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTr
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Squence 1, Application US/10156761

Publication No. US2030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSH1

APPLICANT: ISHIKAM, JUN

APPLICANT: SHIEA, TADAYOSH1

APPLICANT: SAFAKIY, YOSHITUXI

APPLICANT: HATTORI, MASAHIRA

ITTLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT PILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR PLING DATE: 2001-05-30

PRIOR PLING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 1

LENGTH: 9025508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature LOCATION: (4187715)
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      APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/201-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEROTH: 3417
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                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Streptomyces avermitilis
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45.27%
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US-10-156-761-3306
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ç q	38 ASDASpSerSerMetHisGluAlaPheArgGlyLySIleThrAlaLeuTyrAlaLeuGly 57 ::	APPLICANT: OMURA, S. APPLICANT: IKEDA, I APPLICANT: ISHIKAW.
, d	58 ArgThrAsnAsahAspProAsnGlyHisGlyThrHisValAlaGlySerValLeu 77	; APPLICANT: HORINAM; APPLICANT: SHEA, ' ; APPLICANT: SAKAKI, ' APPLICANT: HATTORI
8		; TITLE OF INVENTION: ; FILE REFERENCE: 249 ; CURRENT APPLICATION
g	4132343 GGCACCGGCGCCAAGTCCAACGCCAAGTACAAGGCTGTCGCGCCCGGGCGCGAGGATCCTC 4132284	CURRENT FILING DATE PRIOR APPLICATION N
දු පු	93 PheGlnSerIleMetAspSerSerGlyGlyLeu 103 ::::::    :::    4132283 AACGGCAAGGTCCTCGACGACGACGACGACGACTCCGGCATCTTGGCCGGCATG 413224	, PRIOR FILING DATE: , PRIOR APPLICATION N , PRIOR FILING DATE:
ò	104 -GlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAlaGlyAlaAr 123	; NUMBER OF SEQ ID NO ; SEQ ID NO 5701 ; LENGIH: 3624
Q	4132223 GAGTGGGCGGCCGAGGAGGCGCCGACGTCGTCAACCTGAGCCTGAGCGGGGGGGCGACACC 4132164	, TYPE: DNA , ORGANISM: Streptom
<u>ک</u>	glleHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsnSerArgGl	CDS
<b>a</b> 8		; LOCALION: (17(38 US-10-156-761-5701
전		Alignment Scores: Pred. No.:
ò	nGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLyBAsnAlaIleTh	Score: Percent Similarity: Best Local Similarity:
d d	4132083 CGAAGGCGAGTTCGGCGAGCAGACCATCGGCTCCCCGGGCAGCGCGGCCGACGCTCAC 4132024	Query Match: DB:
5 8		US-09-985-689A-5 (1-43
a :	CGTCGGCGCCC	Qy 8 ValLysAl
충 A	200 BILEATACHTRIBEETSETAIGHTATAINTAGASPOTATAGASPOTATAGASPOTATAGASPOTATAGASPOTATAGASPOTATAGASPOTATAGASPOTAGA	556
ò		18
qq	4131936 CGCACCGGGCGTGGACATCACCGCCGCCGCGGCGCCGGCCGGCGTCATCGA 4131886	9 0 0
δ	240 pAlaAsnTyrAsnSerLygTyrAlaTyrMetGlyGlyThrSerMetAlaTh 257	UV 38 ASILABDSe
qq	4131885 CCAGGAGGTCGGCCAGAAGCCGGACGGCTACCTCACCATCTCCGGTACGTCGATGGCGAC 4131826	
δŏ	leLysAsnArgGlyIl	718
d d	CCCGCATGTCGCGGGCGCCGCCGCATCCTCAAGCAGCAGCACC	Qy 78 Gly
8 4	277 eThrProLysProSerieuIleLysAlaAlaLeulleAlaGiyAlaInfAspva 295	DD 778 GGCAGCGC
g d	CCCAACTGGTCGTTCGCCGAGCTCAAGGGCGCGCGTGACTTCGCGCTTCGCGAAGTCGCAAGTCGCGAAGTCGGAAGTCGGAAGTCGGAAGTCGAAGTCGAAGTCG	Qy 93 PheGlnSe
8 3	235 IGIYUEUGIYIXIFTOSEEGIYABDOINGIYIEDIYAHIYAAINII-EGASDOSEEGE 313 	838
ò	315 uAsnValAlaTyrValAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAlaThrTyrSe 335	
qq	4131672 CAAGCAGTCCGTGATCGCCAACTCGGTGAGCTTCGGCAT-CCAGCAGTGGCCGC 4131614	DD 886 AICGCGG
ζ,	rPheGlnAlaGlnAlaGlyLysPro	946
ا 100	4131613 ACACCGACGACAAGCCGGTCACCCA 4131589	Qy 149 ArgAsnAt
RESI US-1	RESULT 9 US-10-156-761-5701	Db 1006 GAGGAGA

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1006 GAGGAGACGCCCTCTTCGTCGTCGCCGCGGGAAACACCGGTGCCCCCTCC---TCG 1062
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GCCGACATGGCCGAGAGCAGCGCAGATCGGTACGCGGGCCGCGTGGGACGCC 615
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KT, YOSHIYUKI
ON: WONELYUKI
ON: WONEL POLYNUCLECTIDES
249-262
100. NUMBER: US/10/156,761
ATE: 2002-05-29
N WUMBER: JP 2001-204089
E: 2001-05-30
NUMBER: JP 2001-272697
E: 2001-08-02
NOS: 15109
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6918813 GTCGAGGCCGACATGGCCGAGAGGAACGCGAGATCGGTACGCGAGGCCGCGTGGGACGCC 6918872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 GlualaThrAlaLeuAlaThrGlyGlnLysAlaThrTyrSerPheGlnAlaGlnAlaGly 341
                   IleSerAlaProGlyThrAlaLysAsnAlaIleThrValGlyAlaThrGluAsnTyrArg 188
                                                                                                                                                                                                                                                                                                                                                                               268 ArgGluHisPhelleLysAsnArgGlyIleThrProLysProSerLeuIleLysAlaAla 287
                                                                                                                                                             209 AlaThrArg---AspGlyArgIleLysProAspValThrAlaProGlyThrPhelleLeu
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                                                                                        189 ProSerPheGlySerLeuAlaAspAsnProAsnHisIleAlaGlnPheSerSerArgGly
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: OSHINYER:
APPLICANTON: NOVEL POLYNUCLEOTIDES
FILE REFERRENCE: 249-226
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SENOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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Oy 288LeullehlaGlyAlaThrAspValGlyLeuGlyTyProSerGlyAspGlnGly 305  Db 6919626 GAGCAACTCGACGCCTCGGTATATCAGTTGGGGGCGGGTCGGTC	RESULT 11 US-10-090-624-5 Sequence 5, Application US/10090624 Sequence 5, Application US/10090624 Publication No. US202013233A1 GENERAL INFORMATION: APPLICANT: TACKNURA, HINARY APPLICANT: SHINGJO, TOMOKO APPLICANT: SHINGJO, TOMOKO APPLICANT: KATO, INUNOSHIN TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE FILE REPRESENCE: TACKNURA=6 CURRENT FILING DATE: 2002-03-06 CURRENT FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1997-12-06 PRIOR FILING AMER: 1997-06-10 NUMBER OF SEQ ID NOS: 33 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO S LENGTH 4765 TYPE: DA ORGANISM: Artificial Sequence PRATURE: OTHER INFORMATION: Synthetic	Alignment Scores:

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PhealaalaglyAsnGluGlyProAsn --- SerGlyThrIleSerAlaProGlyThrAla 175
                   GTCGCGGCCGGCAACGATGCGTCCAATGTGTCCGGT-----TCGCTGCCGGCCAACTGC
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                                                      LysAsnAlaileThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerLeuAla
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Publication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WEITNAUER, GABRIELE
APPLICANT: TREFZER, AKEL
APPLICANT: TREFZER, AKEL
APPLICANT: RECHTHOLD, ANDREAS
ITLE OF INVENTION: AVILAMYCIN DERIVATIVES
PILE REPERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
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                                                                           Publication No. US20030036176A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Ramseier, Thomas M.
TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris
FILE REPERENCE: 38-10(15824)B
CURRENT APPLICATION NUMBER: US/09/927,827
CURRENT APPLICATION NUMBER: US 60/279,493
RICR APPLICATION NUMBER: US 60/279,493
NUMBER OF SEQ ID NOS: 69
SEQ ID NOS: 69
LENGTH: 3743
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TCGCTCGGCGGCGGCGGTAGCTGCTCGACCACCATGCAGAACGCC---ATCAACGGTGCG
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                   ---GlnLysTyrValGlyAsn 382
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Best Local Similarity:
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APPLICANT TREFER, AXEL
APPLICANT BECHTHOLD, ANDEAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REPERENCE: 1974-005
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN VEY: 3.2
SOFTWARE: PATENTIN VEY: 3.2
LENGTH: 59816
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US-10-084-846A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrSe 254
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Mismatches:
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           PCT/EP01/09815
PRIOR APPLICATION NUMBER: PCT/BE
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 3.2
LENGTH: 1560
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Oy 381 yAsnAspPhes  Db 57601 CAAG7  Qy 401  PheileAsn	RESULT 15 US-10-084-846A-2/C ; Sequence 2, Application; Publication No. US2004(C); GENERAL INFORMATION: APPLICANT: WEITHAUER, APPLICANT: TREFEER, APPLICANT: TREFEER, APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: BEGHTHOLD. TITLE OF INVENTION: APPLICATION: APPLICANTION: APPLICANTION: APPLICATION: APPLICATION NO. CURRENT APLICATION NO. CURRENT APPLICATION NO. CURRE	PRIOR APPLICATION NUM ; PRIOR FILING DATE: 20; PRIOR PELING DATE: 20; NUMBER OF SEQ ID NOS: SOFTWARE: PATENTIN VE; SEQ ID NO 2 ; LENGTH: 59816 ; TYPE: DATE CORGANISM: Streptomyclus-	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	US-09-985-689A-5 (1-433)  QY 21 GlyGlnGlyG  Db 3169 GGGCAGGAGA  QY 41 SerMetHieG	Db 3127 ATCACCACA Cy 60 ASNASNAIAA Cy 60 ASNASNAIAA Db. 3067 AACACGCCC CY 80 AlaLeuAsnL	Db 3007 GCTAC Oy 100 Ser Db 2953 TCGGGCAGG Qy 118 TrpAsnAlaG Db 2893 GT-CAAGCCG Qy 137 TThrAlaAsn Db 2849 CACGGCC Db 2849 CACGGCC	
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	57601 CAAGTC	GTACGGCACCAGCAGCTTCGGACAACATCAACACCCACGTACTCGGT 57654
4.9	[Anstelledor 104	GlyThrTyrThr1leGluVal 415
	S7655 GAACGCCTCCTCGAAGGCGGCC	ហ
608	RESULT 15 US-10-084-846A-2/c ; Sequence 2, Application US/10084846A	
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967	; CURRENT APPLICATION NUMBER: US/10/084,846A; CURRENT FILING DATE: 2003-02-25; PRIOR APPLICATION NUMBER: PCT/EP01/09815	
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072	; SEQ ID NO 2 ; LENGTH: 59816 : TYPE: DNA	
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231	Qy 21 GlyGlnGlyGlnValValAlaValAlaAspT	Ù.
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282	Qy 41 SerMetHisGlualaPheArgGlyLysIleThrAlaLeuTyr	<pre>fhralaLeuTyrAlaLeuGlyArgThr 59 i::</pre>
	Db 3127 ATCACCCÁCAGGGACTTÓGGCGGCCGGGCTCCTACGGCTAÓGACGCCATGGACAACGAC	m
342	Qy 60 AsnAsnAspProAsnGlyHisGlyThrHisValAlaGlyGerValLeuGlyAsn	
H .	80 AlaLeuAsnLys	ABRILEUVAl PheGlnSerIleMetAspSer 99
· .	3007 GCCTAC	:::    :::    :::    GCCTCCCCCCCTCAACAAC 2954
420 .	Qy 100 SerGlyGlyLeuGlyGlyLeuProS	-GlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAla 117
S	Db 2953 TCCGGCCAGGGCACCACCGCCCAGGTCGTCGCCGGCATCGACTCGCCCGGAACGC	sccescarceacrescresces 2894
480	Qy 118 TrpAsnAlaGlyAlaArglleHisThrAsnSerTrpGlyAlaPro-ValAsnGlyAlaTy	
	Db 2893 GT-CAAĠĆĊĠĠĊCGTĊĠĊCAAĊÀÏ	C)
540	Qy 137 rThrAlaAsnSerArgGlnValAspGluTyrValArgAsn	AsnAspMetTh
-	Db 2849 CACGGCCCTCGACACGGCC	
009	Qy 154 rValLeuPheAlaAlaGlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyTh	oAsnSerGlyThrIleSerAlaProGlyTh 174

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Search completed: April 5, 2004, 00:57:57 Job time: 6868.25 secs

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CC Contig67 Conidiobolus cornatus ARSEF 512 Conidiobolus coronatus ARSEF 512 Conidiobolus coronatus AGC 711.
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BUG115128 UI-M-FW0-
BUG115128 UI-M-FW0-
BUG11618 AGENCOURT
AJ773097 AJ77303
CF731090 UI-HF-BN0
BUG11618 AGENCOURT
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                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Conidiobolus coronatus
Eukaryota; Europi Zygomycota; Zygomycetes; Entomophthorales;
Ancylistaces; Conidiobolus.
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-DESCO_SPOOL/USO9985689/runat_31032004_161807_4168/app_query.fasta_1.3498
-DESC_OFVT=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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                            GenCore version 5.1.6
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bh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., ama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., atsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., noue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Ikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., camatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. ad sequence analysis (RISA) system -- 384-format 11, 1757-1771 (2000)
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DGVVITQTFKDQGLEVLKQETAVVBNYPIIGHYQIPSEGGAP VLYSDSNCLDDSHRQ
KDCFWLLDALLQYTSYGYPPPSLSHSNRQPPPSGGAPPBRMEGNHLHRYSKVLEA
HLGDPKPRPLPACPHISWAKRQPLNETAPSNIWKHQKLLSIDLDKVVLDFRSNRPQY
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                                                                                                                                                                                                                                                  2052 GAAGTGGCCTTCTCCTACTCCTCAGTGTTGTGGCCCTGGTCAGGTTACCTTGCCATCTCC 2111
                                                                --- AGCAGC 1847
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                                                                                                                                                                   1848 TATAAACCGCAGGCAAGCCTG---AGTCCTAGCTACATCGACCTGACTGAGTGTCCCTAC 1904
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SM Dictyostelium discoideum

Dictyostelium discoideum

Eukaryoti, Mycetoza, Dictyostelium.

Eukaryoti, Mycetoza, Dictyostelium.

Eukaryoti, Mycetoza, Dictyostelium.

Full length oDNA of Dictyostelium discoideum at the slug stage

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length oDNA of Dictyostelium discoideum at the slug stage

Urushihara, H. Tanaka, C. Dictyostelium discoideum at the slug stage

Contact: Tadasu Shin-i

Contact: Tadasu S
                                                                                                                                                                                                                                                                                                                                                                                                     PheSerTyrProTyrAspAsnAsnTrp------AspGlyArgAsnAsnVal 398
                                                                                                                         348
                                                                                                                                                                                                                  -----ThrLeu 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 GluAsnValPhe------IleAsnAlaProGlnSerGlyThrTyrThrIleGlu 414
                                                                                                                                                                                                                                                                                                              364 ValAsnAspLeuAspLeuValIleThrAlaProAsnGlyGlnLysTyrValGlyAsnAsp 383
                                  SerteuAsnValAlaTyrValAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAlaThr 333
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'clone_lib="Dictyostelium discoideum cDNA library, SF"
                                                                                                                         TyrserPheGlnAlaGlnAlaGlyLysProLeuLysIleSerLeu-------
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/mol_type="mRNA"
/strain="AX4"
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Conservative:
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Indels:
Gaps:
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clone="dds32b16"
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Best Local Similarity:
Query Match:
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VERSION
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AUTHORS
TITLE
JOURNAL
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BJ393752
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EST 08-MAR-2002
Dictyostelium
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                                                                     83 -----LysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSerSer
                                                                                                                                               137 TyrThralaasnSerArgGlnValAspGluTyrVal---ArgAsnAsnAspMetThrVal
21 AAAGTIGTAACTTATATTACCACATCAACAAGCGACGATAGTGGATAAGTGGATGGTCAC
                                                                                                                                                                                             101 GlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAla
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                                                 --AsnAlaLeuAsn----
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/clone lib="Dictyostelium discoideum cDNA library,
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Dictyostelium discoideum
Eukaryota, Myctozoa, Dictyosteliida, Dictyostelium.
Eukaryota, Myctozoa, Dictyosteliida, Dictyostelium.
1 (bases 1 to 640)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostellum discoideum at the sluu bubblished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@gene8.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ395336 Bictyostelium discoideum cDNA library, SF discoideum cDNA clone dds38b16 5', mRNA sequence.
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                                                 GlyThrHisValAlaGlySerValLeuGly----
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Matches:
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/clone="dds38b16"
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/strain="AX4"
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BJ395336.1 GI:19306422
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il: ff4@ummail.und.edu.
Location/Qualifiers
1. 2141
| ...2141
| /organism="Wetarhizium anisopliae var. acridum"
| mol_cype="mmRNA" | / for aref="taxon:92637" | / folone lib="Metarhizium anisopliae sf. acridum ARSEF 324" | / folone lib="Metarhizium anisopliae sf. acridum ARSEF 324" | / folone lib="Metarhizium anisopliae sf. acridum was grwon on insect cuticle and chitin for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector Unizap."
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GGTGAGGGTACTTGCGTATATATTGACACTGGTGTTGAGGTCTCC------
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Tel: 301 Fax: 301 Email: ff
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Prelmoser.F.M., Screen,S., Baga,S., Hu,G. and St. Leger,R.J.
Stranalyais of genes expressed by two different insect pathogenic fundi during optimized secretion of proteins
Unpublished (2002)
Contact: Freimoser F. M.
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                                                                                                                                                                       -SerMetHisGluAlaPheArgGly
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Metarhizium anisopliae var. acridum
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hyporeomycetidae; Hyporeales; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
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University of Maryland
4112 Plant Sciences Building,
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Glibberella zeae cDNA clone F902_10908, mRNA sequence.
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Bukaryota, Fungi, Hypocreales, Nectriaceae, Gibberella.

1 (Dases 1 to 718)
Harris, L.J., Glassco, T., Rocheleau, H., Allard, S., Chapados, J.,
Couroux, P., De Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S.,
Singh, J.A, Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Fusarium graminearum mycelium
Unpublished (2001)
AsnAlaGlyAlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyrThr
                                            158 AlaAlaGlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsn
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Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KIA OC6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harris1@em.agr.ca.
Location/Qualifiers
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Direct Submission

Hillorect Sunger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a closed population of Trypanosoma brucei (TREU9274 GUTat 10.1) was mechanically sheared to give a tight size distribution (
Trypanosoma brucei (TREU9274 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Ganome Sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

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                                            MetalaThrProlleValAlaGlyAsnValAlaGlnLeuArgGluHisPhelleLysAsn 274
                                                                                            ATGCTACTCCCCATATTGCTGGT-----CTTGCTGCCTACTTCAGTGCTCTC 424
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/mol_type="genomic DNA"
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UI.MFWO.cby-d-23-0-UI.rl NIH BMAP_FWO Mus musculus cDNA clone
UI.MAGE.6816072 5', mRNA sequence.
CA320325
CA320325.1 GI:24538449
EST.
Mus musculus (house mouse)
liquid nitrogen prior it's storage at -80 C until RNA extraction. Directional cloning with 5' end of CDNA cloned into EcoRI site of pBluescript and 3' end of CDNA cloned into XhoI site of pBluescript (Stratagene, La Jolla, CA)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 771)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lih, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://mage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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SF.

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BUS75479

SASTAYABODO7. Y1 TGVEG Partially sporulated cocyst cDNA TOXOD1asma gondii cDNA clone TgESTZYABODO7. Y1 5' similar to TR:Q45522 Q45522 PREPRO-SUBTILLSIN SENDAI PRECURSOR.;, mRNA sequence.

BUS75479.1 G1:23045230
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Toxoplasma gondia

Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;

Eukaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocyetidae; Toxoplasma.

1 (Dases 1 to 545)

Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,

Tang,K., Cole,R., Marera,M.,

Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,

Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,

Kennedy,S., Maquire,L., Waterston,R. and Wilson,R.

Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 TTAGTTGATGGTTATTATCCAACTGGTTCAATTGTAGAATCAAATAAAATTACAACT
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405 TTGATTACATCAAGTATTACATATCCATCAAACCAAGTTTTTGAAAATTTTGCAGGT
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                                                                                                                                                                                                                                                                                                                                                                               ProAspValThrAlaProGlyThrPhelleLeuSerAlaArgSerSerLeuAla-----
/sex="mat A"
/dev_stage="Slug stage"
/clone_lib="Dictyostelium discoideum cDNA library,
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                               (1-601)
                                                                                                                                                                                                                                                                 US-09-985-689A-5 (1-433) x BJ387574
                                                                                                                3.78e-09
193.50
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33.54%
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91387574 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds3al8 5', mRNA sequence.
BJ387574
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                                                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                         ThrvalGlyAlaThrGluAsnTyrArgProSerPheGlySerLeuAlaAspAsnProAsn 199
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  LysglyMetAlaProGlnAlaAsnLeu---ValPheGlnSerIleMetAspSerSerGly 101
                         GlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAlaGly
                                                                                                              -------GIGICITACACAICITGGITICTGGAIGCCTICAACTAIGCC
                                                                                                                                                                                                  340 ATCCTAAAGAAGATGGACGTTCTCAACCTTAGCATCGGTGGGCCCGACTTCATGGATCAT
                                                                                                                                                                                                                                              142 ArgGlnValAspGluTyr-----ValArgAsnAsnAspMetThrValLeuPheAlaAla
                                                                                                                                                                                                                                                                     GlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIle
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                                                                                                                                                           122 AlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsnSer
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Dictyostelium discoideum

Dictyostelium discoideum

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Dictyostelium discoideum

Lobace 1 to 601)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Contact: For Genetic Resource Information

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/organism="Dictyostelium d:
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clOne="dds3a18"
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Spendic brucei sheared genomic DNA clone 315h10, forward sequence,
AL490202
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                                                                176 LysasnalaileThrvaiGlyalaThrGluasnTyrargProSerPheGlySerLeuala 195
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    -----CAGTTTCGCGAACTTTCCGGAACCTCCATG
                                                                                                                                                                                                                                         216 LysProAspValThrAlaProGlyThrPheIleLeuSerAlaArgSerSerLeuAlaPro
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                         256 AlaThrProIleValAlaGlyAsnValAlaGlnLeu 267
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mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="315h10"
                                                                                             AL490202.1 GI:11866292
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1 (bases 1 to 574)
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Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Foxogwatson.wastl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40Rp from Gibco
High quality sequence stop: 445.
Location/Qualifiers
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Alignment Scores:

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BZ424995
100023066-5726 Aspergillus terreus random genomic DNA clone library
Aspergillus terreus genomic, genomic survey sequence.
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Aspergillus terreus
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales, Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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                                                                                                   GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArgAsnAspSer
                                                                                                                                               41 SerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAlaLeuGlyArgThrAsn
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|GGTCAGGGTACTTGCGTATATATCATTGACACTGGTATTGAG----
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Length:
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1 (Dases 1 to 2121)
Askenazi,M., Driggers,E.M., Holtzman,D.A., Norman,T.C., Iverson,S.
Zimmer,D.P., Boers,M.E., Blomquist,P.R., Martinez,B.J.,
Monreal,A.W., Feibelman,T.P., Mayorga,M.E., Maxon,M.E., Sykes,K.,
Tobin,J., Cordero,E., Salama,S.R., Trueheart,J., Royer,J.C. and
Madden,K.T.
                                                                        Integrating transcriptional and metabolite profiles to direct the engineering of lovastatin-producing strains Unpublished (2002) Contact: Zimmer DP Microbia, Inc. One Kendall Square Building 1400 W, Cambridge, MA 02139, USA Fax: 617-621-8322 Fax: 617-Email: dzimmer@microbia.com
                                                                                                                                                                                                                                          /organism="Aspergillus terreus"
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db_trei="texpon:33179"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae, Murinae; Musmanila; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus. 1 (bases 1 to 655)

Rodentia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 655)

Rational Institutes of Health, Mammalian Gene Collection (MGC)

Au Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov, Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. Jim Lih. M. Bento Soares, University of Iowa DNA Sequencing Dy: Dr. M. Bento Soares, University of Iowa DNA Sequencing Dy: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC Clone distribution information can be found through the I.M.A.G.B. Consortium/Linl. at:

http://image.llhl.gov

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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/clone="IMAGE:5702970"
/clone="IMAGE:5702970"
/dev_stage="embryo 12.5dpc"
/lab host="Filt10B (TI phage resistant)"
/clone lib="NIH BMAP F10"
/note="Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
/note="Torgan: Brain; Vector: pXX-
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UI-M-FIO-byv-m-19-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:5702970 5', mRNA sequence.
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----AlaProGly-ThrAlaLysAsnAlaI
                                                                                                                                                                                                                            Seq primer: pYX-5.
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/ organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6"
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Halorubrum lacusprofundi
Halorubrum lacusprofundi
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with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Descioping Mouse Nervous System', supported by National Institute of Mantal Health (NIWH), Hemin Chin, Ph.D., program coordinator."
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701 TCCGATGCGTCGGACGNAGACGGGCACGGAACTCACGTCGCCGGAACCGTCGCGGGA
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Archaear Buryzchaecta; Halobacteria; Halobacteriales; Halobacteriaceae; Halorubrum.

I (bases 1 to 716)

Goo, Y., Road, J., Glusman, G., Baliga, N.S., Deutsch, K., Pal DasSarma, S., Ng, W.V. and Hood, L.

Low-pass Sequencing for Microbial Comparative Genomics Unpublished (2003)

Contact Goo Y.

Institute for Systems Biology
Institute for Systems Biology
Tel: 206 732 1412
Fax: 206 732 1412
                                                                                                                                                                                                                                                                                                                                                                          /organism="Halorubrum lacusprofundi"
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                                                                                                                                                                                                                                                                   Email: ygoo@systemsbiology.org
Seg primer: M13 Forward
Class: shotgun.
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Search completed: April 4, 2004, 11:55:04 Job time : 2283.58 secs

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/clone lib="Metarhizium anisopliae ARSEF 2575" note="Vector: Unizap, Metarhizium anisopliae was grown on insect cuticle for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector, Unizap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                (hases 1 to 614)
Screen,S.E., Mathur,P. and St. Leger,R.J.
Stranslysis of the insect pathogenic fungus Metarhizium anisopliae
Unpublished (1999)
Contact: Screen SE
                                                                                                                                                                                                              AJ273402 Metarhizium anisopliae ARSEF 2575 Metarhizium anisopliae CDNA clone Ma#948, mRNA sequence.
AJ273402
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                        ....-CAGTTTCGCGAACTTTCCGGAACCTCCATG 501
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AspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrSerMet
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AJ273402.1 GI:6432774
Metarhizium anisopliae
Metarhizium anisopliae
Metarhizium anisopliae
Bukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypooreomyetidae; Hypooreales, Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
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University of Maryland
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA.
Location/Qualifiers
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SETAÎN="ARSEF 2575"
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Dictyostelium
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Dictyostelium discoideum

EMARATOGE, Mycebacza; Dictyosteliida; Dictyostelium.

EMARATOGE, Mycebacza; Dictyosteliida; Dictyostelium.

E 1 (bases 1 to 601)

S Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length CDNA of Dictyostelium discoideum at the slug stage tungublished (2002)

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Contact: Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.
                                                                                                   651
                                                                                                                                           hralaLysAsnAlaIleThrValGlyAla------ThrGluAsnTyrArgP 189
                                                                          roSerPheGlySerIleAlaAspAsnProAsnHisIleAlaGlnPheSerSerArgGlyA 209
                                                                                                                          laThrArgAspGlyArgIleLysProAspValThrAlaProGlyThrPheIleLeuSerA 229
                                                                                                                                                                            laArgSerSerLeuAlaProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaT 249
                                                                                                                                                                                                     249 yrMetGlyGlyThrSerMetAlaThrProlleValAlaGlyAsnValAlaGlnLeuArg- 268
                                                                                                                                                                                                                                                                              ----GluHisPheileLysAsnArgGlyileThrProLysProSerLeuileLysAlaA 287
                                                                                                                                                                                                                                                                                               526 CGCTGGAGGACCTCAGCAGCCCCAAGGCCGTCACTGACCGC-----ATCAAGGAGC 476
TGGAGTGCGGACTCCGCTGACTGATTCGACAGACCGACGCCTCGAGCACCAGCCCGGCTT 731
                                                                                                                                                                                                                                              SF
                                        /dev_stage="Slug stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                    BU387574 601 bp mRNA linear BU387574 Dictyostelium discoideum cDNA library, SF 1 discoideum cDNA clone dds3a18 5', mRNA sequence. BU387574 GI:19296958
                                                                                                  670 CCAACTACGGCTCCGTGGTG------
                                                                                                                                                                                                                                                                                                                             287 laLeuIleAlaGlyAlaThrAspValGlyLeuGlyTyrProAsn 301
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mol type="mRNA"
strain="AX4"
/db xref="taxon:44689"
/clone="ddg3a18"
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BUS75479.1 GI:23045230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for further clone availability.
                                                                                                                                                                                                    345 GGATCATTAATAAAAGCATTAATGATTAATAATAATAATGCTCAGTTATTAAATGGTACATTTCAA 404
234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 TCTGGTACATCAATGGCAACCTCATTTGCAGCAGCAACAACAACAATTCTTAGACAATAT 284
                                                                                                                                         ProAspValThrAlaProGlyThrPheIleLeuSerAlaArgSerSerLeuAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 ProSerLeuIleLysAlaAlaLeuIleAlaGlyAla------------------
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/mol_type="mRNA"
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Madden, K.T.  Integrating transcriptional and metabolite profiles to direct the engineering of lovastatin-producing strains  JOURNAL Unpublished (2002)  COMMENT Contact: Zimmer DP  Microbia, Inc.  CORREST: Zimmer Building 1400 W, Cambridge, MA 02139, USA  Tel: 617-621-8322  Class: 617-  Enail: dzimmer@mid cncm  Class: incation/Qualifiers  1. 2121  /mol type="genomic DNA"  /strain="APCC 20542 (A. terreus Thom, anamorph)"  /mol type="genomic DNA"  /strain="APCC 20542 (A. terreus Thom, anamorph)"  /mol type="letaxon:33178"  /mol type="Entaxon:33178"  /lab host="Escherichia coli"  /clone lib="Aspergillus terreus random genomic DNA clone library"  /note="Wetcor: PZETOTM-2; Site 1: Sau3A; Site 2: BamHI; Sau3A genomic fragments ligated into BamHI digested  pZETOTM-2 "	Alignment Scores: Pred: No:: 192.00	Qy         96 Ile-MetAspSerSerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsn
0y 28 ValaladspThrGlyLeuAspThrGlyArgAsnAspSerSerMetHisGluAlapheArg 47	0y 142 ArgGinValAspQluTyrValArgAsnAsnAspMetThrValLeuPheAlaAla 159  400 CCGTTTGTTGACAAGGTGTGGGAATTACAGCTAATTATGGTTTTGGTATT 459  160 GlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIle 179  460 GGCAATGATGGCTTCTTATGGACTTCTGAATAACCTGTGATT 519  180 ThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIleAlaAspAsnProAsn 199  180 ThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIleAlaAspAsnProAsn 199  180 ThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIleAlaAspAsnProAsn 199  180 ThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIleAlaAspAsnProAsn 199  200 HislleAlaGlnPheSerSerArgGlyAlaThrArg	Db 691 ÀGTGTCGCTTCCCCAGTGGCGGCGTCACCTTGTTÀGTANGCACAGTACAGÀG 750  Oy 274 AsnArgGlylleThrPro 279  Db 751 CGGAGCTGGTGAATCCT 768  RESULT 9  BZ424995

553 254 -----TGG-----ATCAAIGGCCGCACCAACACCATCTCTGGCACCTCCC 472 MetAlaThrProlleValAlaGlyAsnValAlaGlnLeuArgGluHisPhelleLysAsn 274 615 GICGCCGCTGGCAACGATAACCGGGATGCCCAAAACACCTCT---CCCGCTTCCGAGCCT 619 618 ACTGCCTGCACTGTTGGTGCCACTGCGTCAGATGACACGCCGATCTACCCTTTTCCAACTAC 559 TyrThrAlaAsnSerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeu 156 157 PhehlahlaglyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAlaLys 176 215 IleLysProAspValThrAlaProGlyThrPheIleLeuSerAlaArgSerSerLeuAla 234 275 ArgGlyIleThrProLysProSerieuIleLysAlaAlaLeuIleAlaGlyAlaThrAsp 294 21 GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArgAsnAspSer 40 90 177 AsnalaileThrValGlyAlaThr-----GluAsnTyrArgProSerPheGlySerIle ::: GTT---GTCGATATCTTCGCTCCTGGTACCGGCATTCTCTCCCC-------ATGCTACTACTCCCCATATTGCTGGT-----CTTGCTGCTGCCTACTCAGTGCTCTC 41 SerMetHisGluAlaPheArgGlyLysIleThrAlaLeuTyrAlaLeuGlyArgThrAsn AsnAlaSerAspProAsnGlyHisGlyThrHisValAlaGlySerValLeuGlyAsnAla 81 LeuAsnLysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAsp-----SerSerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAlaTrp AsnalaGlyalaArgileHisThrAsnSerTrpGlyAlaProValAsn-----GlyAla AlaAspAsnProAsnHisIleAlaGlnPheSerSerArgGlyAlaThrArgAspGlyArg ProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrSer 214 880 146 108 134 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-985-689A-4 (1-433) x BQ142519 (1-2141) 5.15e-09 200.00 43.75% 27.78% 8.85% Percent Similarity: Best Local Similarity: Query Match: DB: 235 471 61 66 137 195 552 510 255 906 119 735 558 Pred. No.: qq g ጵ 심장 음 상 음 8 8 8 원 장 임 ò ď 셤 ઠે 셤 ઠે ò 셤  $\dot{\delta}$  $\delta$ à ď ò

/uringlain="Mus musculus"
// proganism="Mus musculus"
// proganism="mus musculus"
// progani="CSTBL/6"
// db xref="taxon:10090"
// clone="IMAGE:6816072"
// tissue\_type="manbo"
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// lab\_host="mubyo lis.5,14.5,16.5,17.5dpc"
// lab\_host="mubyo lis.5,14.5,16.5,17.5dpc"
// lab\_host="mubyo lis.5,14.5,16.5,17.5dpc"
// clone lib="muhy lamap Few"
// lab\_host="muhyo lis.5,14.5,16.5,17.5dpc"
// note="Organ: Brain, Vector: pyx- Asc; Site\_1: EcoR I;
Site\_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:191-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pix-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGGAGAGACAG. This library was created for the University
lows Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator:" CA320325 UI-M-FWO-Cby-d-23-0-UI.rl NIH\_BMAP\_FWO Mus musculus CDNA clone IMAGE:6816072 5', mRNA sequence. Length:
Matches:
Conservative:
Mismatches: 5.26e-09 192.50 39.86% 26.92% 8.52% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 363 ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 8 CA320325 LOCUS DEFINITION Pred. No.: REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES DRIGIN

27

ValLysAlaAspValAlaGlnAsnAsnTyrGlyLeuTyrGlyGlnGlyGlnValValAla

US-09-985-689A-4 (1-433) x CA320325 (1-771)

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ValGlyLeuGlyTyrProAsnGly 302

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SerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGly
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/mol type="mRNA"
/pre="mRNA"
/pre="mRNA"
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/db xref="taxon:518"
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/clone_lib="Fg02 AAPC_ECORC_Fusarium_graminearum_mycelium"
/note="Vector: Bluescript SK+/KhoI-ECORI, Site_1: EcoRI,
Site_2: XhoI; Mycelial tissue was collected from VB agar
plates after a growth period of 6-7 days at 25 C with 14
hrs (FL/UV) day lighth exposure. Mycelia was ground in
liquid nitrogen prior it's storage at -80 C until RNA
extraction. Directional cloning with 5' end of cDNA cloned
into EcoRI site of pBluescript (Stratagene, ia Jolla, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 AlaProGlnAlaAsnLeu------ValPheGln---SerIleMetAspSerSer 100
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                                                                              Gibberella zeae
Gibberella zeae
Gibberella zeae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
I (bases I to 718)
Harris, L.J., Glassco, T., Rocheleau, H., Allard, S., Chapados, J.,
Courow, F., De Moors, A., Hattori, J. I., Ouellet, T., Robert, L.S.,
Singh, J.A, Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Fusarium graminearum mycelium
Unpublished (2001)
                                                                                                                                                                                                                                                       Contact: Harris, Linda J.

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, KlA 0C6,
CANADA
Fg02 10g08 R Fg02 AAFC ECORC Fusarium graminearum mycelium Gibberella zeae cDNA clone Fg02_10g08, mRNA sequence.
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Location/Qualifiers
                                                        BI750157.1 GI:15771959
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28.37%
8.85%
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Fax: (613) 759-6566
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BQ142519 24-APR-2002 Contig6 Metarhizium anisopliae sf. acridum ARSEF 324 Metarhizium anisopliae var. acridum cDNA, mRNA sequence.
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TTCAACAACGCTGTCGAGTCTKCYTCCAGCTCCGGTATTATCTCTGCCATTGCTGCCGGT
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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
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                                                                                                                                                                                                                                                                            175 AlaLysAsnAlaIleThrValGlyAlaThrGluAsnTyrArgProSerPheGlySer--- 193
                                                                                                                                                            LeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArg--- 37
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Traagaggtaaaggtcagatattgagtattgctgatactggtttagatggtagccattgt 81
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Constructed at the Institute for Genomic Research (TIGR),
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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TyralaLeuGlyargThrAsnAsnAlaSerAspPro---AsnGlyHisGlyThrHisVal
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Pred. No.:
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BJ395336
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                                                                                                                                                              1904
                                                                                                                                                                                                                                      --- AGCAGC 1847
                                                                                                                                                                                                                                                                                                                                        1956 GTTAAT-----GTCACCATCCTCAAGGCATGGCGTCACAGGAGAATT 2000
                                                                                                                                                                                                                                                                                                                                                                                                                  2052 GAAGTGGCCTTCTCCTACTCCTCAGTGTTGTGGCCCTGGTCAGGTTACCTTGCCATCTCC 2111
                                                                                                                                                                                                                                                                                                                                                                                        398
                                                                                                                                                                                                         -----ThrLeu 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 GluAsnValPhe-------IleAsnAlaProGlnSerGlyThrTyrIleIleGlu 414
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SM Dictyostelium discoideum

Dictyostelium discoideum

Dictyostelium discoideum

E Ukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

E Uruchinara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the slug stage

Corteact: Tadaeu Shin-i

Conteact: Tadaeu Shin-i

Center For Genetic Genetics

Ill Yata, Mishina, Shizuoka 411-8540, Japan

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                          SerLeuAsnValAlaTyrValAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAlaThr 333
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/clone_lib="Dictyostelium discoideum cDNA library, SF"
                                                                                                                                                              1848 TATAAACCGCAGGCAAGCCTG---AGTCCTAGCTACATCGACTGACTGAGTGTCCCTAC
                                                                                                                                                                                                                                                                                                                                                                                        384 PheSerTyrProTyrAspAsnAsnTrp------AspGlyArgAsnAsnVal
                                                                                                                334 TyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIleSerLeu----
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Mismatches:
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clone="dds32b16"
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                                                                       1827 GCTTATCAGATCCTC--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AlaileThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIleAlaAspAsn 197
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Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
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S Urushinara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
S Urushinara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill Yake Mashima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
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                                                                                                                                                                                                          MetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSerSerGlyGlyLeuGly 104
72
                                 ||| :::||||||||||||| 92 |
33 TATATTACCACATCAAGAGAGATAAGTGATAAAGTGGATCACGGTACACATATT 92
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BJ395336 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds38b16 5', mRNA sequence.
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/clone_lib="Dictyostelium discoideum cDNA library, SF"
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/mol_type="mRNA"
/strain="AX4"
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Matches:
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/clone="dds38b16"
/sex="mat A"
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Location/Qualifiers
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AUTHORS

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1305 ATCCTAAAGAAGATGGACGTTCTCAACCTTAGCATCGGTGGGCCCGACTTCATGGATCAT 1364
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                                                                                                                                                                                                                                                                                                                                                     28 ValAlaAspThrGlyLeuAspThrGlyArgAsnAspSerSerMetHisGluAlaPheArg
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1572 | CGTGTGAAGCCTGACATTGTCACCTATGGTGCTGGAGTGCGGGGT--------
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113
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168
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21
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                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                      5.61e-11
224.00
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Percent Similarity:
Best Local Similarity:
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, N., Hayasu, N., Hiramco, T., Hiracan, T., Hiracan, T., Hayasu, T., Hayasu, T., Hiracan, T., Hayasu, T., Imotani, R., Ishii, Y., Itch, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Itch, M., Kagawa, I., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Musata, M., Ohasto, M., Okazaki, Y., Saski, N., Nomura, K., Ohno, M., Ohasto, M., Sano, H., Saski, D., Shibata, K., Shiraki, T., Sakai, Y., Tagami, M., Tagawa, A., Takahashi, F., Takau-Akahira, S., Muramatsu, M. and Hayashizaki, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Vasunishi, A., Muramatsu, M. and Hayashizaki, Y., Direct Submission

L. Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, Exploration Research Group, Kinken Golence Exploration Research Group, Riken Geneme Exploration Research Group, Fax: 91-45-503-9216,

CDNA library was Drepared and sequenced in Mouse Geneme Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genome Royase mouse tissues.

Plasse wish to use the search in Riken contributed to prepare mouse tissues.
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/clone lib="Conidiobolus cornatus ARSEF 512"
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S Freimoser, F.M., Screen, S., Hu, G. and St. Leger, R.J.

EST analysis of genes expressed by the zygomycete pathogen
Conidiobolus coronatus during optimized secretion of proteins
Unpublished (2002)
Concact: Freimoser F. M.
University of Maryland
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301 314 405 16
Fax: 301 314 92 90
Email: ff84@umail.umd.edu.
Location/Qualifiers
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4198 bp mRNA linear HTC 18-SEP-2003
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732484M11 product:membrane-bound transcription
Eactor protease, site 1, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4198)
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Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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April 3, 2004, 23:40:05; Search time 2274:58 Seconds (without alignments) 5684.703 Million cell updates/sec
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Maximum Match 100%
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Fgapop 6.0, Fgapext (
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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	s	361 rThrieuValAsnAspLeuAspLeuVallleThrAlaProAsnGlyGlnLysTyvalGl :    :::        :::	381 yAsnAspPheSerTyrProTyrAspAsnAsnTrpAspGlyArgAsnAsnValGlus	Oy 401   PhelleAsnAlaProGinSerGir/hrryzileileGiuval 415 	RESULT 15 US-10-084-846A-2/c ; Sequence 2, Application US/10084846A ; Publication No. US20040006026A1	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: WILLENWEG, AGNES APPLICANT: TREFERR, AKEL	; APPLICANT: BENTHALD. I ANDREAS; TILLS OF INVENTION: AVILANYCIN DERIVATIVES; FILE REFERENCE: 1974-005; CURRENT APPLICATION NUMBER: US/10/084,846A	CORKENT FILING DATE: 2003-02-25 ; PRIOR APPLICATION NUMBER: PCT/EF01/09815 ; PRIOR FILING DATE: 2001-08-24 ; PRIOR PPLICATION NUMBER: DE 101 09 166.4	FRIOK FILING DAIR: 2001-02-62 ; NUVBER OF SEQ ID NOS: 120 ; SOFTWARE: Patentin Ver. 3.2 ; SEQ ID NO 2	tryPE: DNA	ent Scores: 1.44e-20 Length: 5 No.: 298.00 Marches: 1	ercent similarity: %1.14* uery Match: 13.19* 15.19*	G G	Db 3169 GGGCAGGAGTGACGGCGTACGTCATCGACACGGCGTCCGC 3128	3127 ATCACCCACACACCACGCCGGCCGCCTCCTACGGCTACGACGCCATCGACGAC	60 AsnAsnAlaSerAspProAsnGlyHisGlyThrHisValAlaGlySerValLeuGlyAsn	Db 3067 AACACCGCCAGGACGGCCACGGCACGCACGTGGCCGGCGCGCGGTCGCGGGAC 3008   Qy 80 AlaLeuAsnLysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSer 99
; TYPE: DNA ; ORGANISM: Streptomyces viridochromogenes US-10-084-846A-1	Alignment Scores: 1.44e-20 Length: 59816 Pred. No.: 298.00 Matches: 126 Score: 42.11\$ Conservative: 50 Percent Similarity: 42.11\$ Mismatches: 153 Query Match: 13.19\$ Indels: 19 D8: 15	-09-985-689A-4 (1-433) x US-10-084-846A-1 (1-59816) 21 GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArgAsnAspSer 40	Db 56648 GGGCAGGAGTGACGCGTACGTCACACCGCGGCGTC	Oy 60 AsnAsnAlaSerAspProAsnGlyHisGlyThrHisValAlaGlySerValLeuGlyAsn 79	Qy 80 AlaLeuAsnLysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerIleMetAspSer 99	Qy 100 SerGlyGlyLeuGlyGlyLeuProSerAsnLeuAsnThrLeuPheSerGlnAla 117	Oy 118 TrpAsnAladlyAlaArgIleHisThrAsnSerTrpGlyAlaPro-ValAsnGlyAlaTy 137	Oy 137 rThralaabanSerargGlnValaspGluTyrValargAsnAsnaspMetTh 154	Qy 154 rValLeuPheAlaAlaGlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyTh 174	Oy 174 rAlaLysAsnAlaIleThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIl 194	Qy 194 eAlaAspAsnProAsnHisIleAlaGlnPheSerSerArgGlyAlaThrArgAspGlyAr 214 :::   :::    ::: Db 57128 57151	Qy 214 glleLysProAspValThrAlaProGlyThrPheIleLeuSerAlaArgSerSerLeuAl 234	Qy 234 aProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThrSe 254	25 6	Thr ProLysProSerLeuileLysAlaAlaLeuileAlaGl 291	cccrcaccchcccaagrescaragesaragesaragesarccaccaccaccas	Qy 291 yAlaThrAspValGlyTueuGlyTyrProAsnGlyAspGlnGlyTrpGlyArgValThrLe 311

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174 rAlaLysAsnAlaileThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIl 194
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                                                                                                                                                                                   401 lPheileAsnAlaProGln-----SerGlyThrTyrIleIleGluVal 415
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| Publication No. US20040006026A1
| GENERAL INFORMATION: ASPLICANT: WETTNAUER, GABRIELE
| APPLICANT: WHLENNEG, AGNES
| APPLICANT: WHLENNEG, AGNES
| APPLICANT: TREFZER, AXEL
| APPLICANT: BECHTHOLD, ANDREAS
| TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
| FILE REFERENCE: 1974-005
| CURRENT APPLICATION NUMBER: US/10/084,846A
| CURRENT PELING DATE: 2003-02-25
| PRIOR PILING DATE: 2001-08-24
| PRIOR FILING DATE: 2001-08-25
| NUMBER OF SEQ ID NOS: 120
| SOFTWARE: PARENTIN VEY: 3.2
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FOTHER INFORMATION: aviX16 dna: partial sequence of coding strand 1; nucleotide 1; OTHER INFORMATION: corresponds to nucleotide 56,198 of coding strand 1.
US-10-084-946A-113
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: WEITNAUDE, GABRIELE
APPLICANT: WHILENWEG, AGNES
APPLICANT: TEREZER, AXEL
APPLICANT: TEREZER, AXEL
APPLICANT: TEREZER, AXEL
APPLICANT: BECHTHGUD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REPRENCE: 1974-005
CURRENT PELLING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US/10/084,846A
CURRENT PILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 113
    CTGAAGGCCTACAGCACGTTCTCCGGC 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Streptomyces viridochromogenes
                                                                                                  Sequence 113, Application US/10084846A Publication No. US20040006026A1 GENERAL INFORMATION:
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Percent Similarity;
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Qy 89 AlaAsnLeu	100	Cy 117 AlaTrpAsnAladlyAlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAla	Qy         137 TyrThrAlaAsnSerArgGlnValAspGluTyrValArgAsnAsnAspMetThrValLeu           :::         :::           Db         1979 GTGTCGCGCGCACCACGGTGGTG	Cy 157 PheAlaAlaGlyAsnGluGlyProAsnSerGlyThrIleSerAlaProGlyThrAla	Cy 176 LygAsnAlaileThrValGlyAlaThrGluAsnTyrArgProSerPheGlySerIleAla	Qy 196 AspAsnProAsnHisIleAlaGlnPheSerSerArgGlyAlaThrArgAspGlyArgIl  Db 2099AAGGCCAGCTATTCCAACTTCGGCACC	Oy 216 LysProAspValThrAlaProGlyThrPheIleLeuSerAlaArgSerSerLeu	Qy 234 AlaProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyrAlaTyrMetGlyGlyThr	Oy 254 SerMetAlaThrProIleValAlaGlyAsnValAlaGlnLeUArgGluHisPheIleLys	Qy 274 AsnArgGly1leThrProLysProSerLeulleLysAlaAlaLeulle i::	290	Oy 301ABNGlyASPGlnGlyTrpGlyArgValThrLeuABnLySSerLeuABnVal	Oy 318 AlaTyrValAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAlaThrTyrSerPheGln	Oy 338 AlaGlnAlaGlyLysProLeuLysIleSerLeuValTrpThrAspAlaProGlySerThr	Qy 358 ThrAlaSerTyrThrLeuValAsnAspLeuAspLeuVallleThrAlaPro	Oy 375 AsnGlyGlnLysTyrValGlyAsnAspPheSerTyrProTyrAspAsnAsnTrpAspGly	Qy 395 ArgAsnAsnValGluAsnValPheIleAsnAlaProGlnSerGlyThrTyrIleIleGlu
377Aspheser 385	TyrProTyrAspAsnAsnTrpAspGlyArgAsn       Arctatgcaactgaaccatgaattctagaacacatgaattctagaacacatgaataagcctttgtcagtgaaagaactgaagaac	397 AsnValGluAsnValPhe	412	420 ValbroSerGlyProGlnArgPheSer 428 2461 ACAATTGTTATTCCCGAGAAGTTCACT 2487	RESULT 12 US-09-927-827-29 ; Sequence 29, Application US/09927827		TITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris FILE REFERENCE: 38-10(15824)B CURRENT APPLICATION NUMBER: US/09/927,827 CURRENT FILING DATE: 2001-08-10	PRIOR APPLICATION NUMBER: US 60/279,493 PRIOR FILING DATE: 2001-03-28 FOLD NO 29		NAME/KEY: CDS LOCATION: (1001)(2743) -09-927-827-29	1.32e-22 Length: 300.50 Matches: 40.51% Conservati	: 29.42% Mismatches: 13.30% Indels: 10 Gaps:	A-4 (1-433) x US-09-927-827-29 (1-3743)  GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGly	37 ArgAsnAspSerSerMetHisGluhlaPheArgGlyLysIleThrAlaLeuTyrAlaLeu	1562 GCCAACATCCTCGCGGGCTACGACTTCATCAGCGATGCGACCACGGCACGCGATGGCAAC 1621     57 GlyargthrashashalaSerasp	65ProAsnGlyHisGlyThrHisValAlaGlySer	1682 GGCGGCCGGCCGGCCGGCCGGCGCCCGGCCGGCCGGCC

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                                                                                                                                                                  TCAAGACTCTATGGTTGGGATTATACGAACGTTACCACAGACACCGTGCAGGGTGTTGCT 1371
                                                                                                                                                                                                                                                                <u> CCAGGTGCCCAAATAATGGCAATAAGAGTTCTTAGGAGTGATGAA-----CGGGGTAGC 1425</u>
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                                                                                                                                                                                                                                                                                             uAsnValAlaTyrValAsnGluAlaThrAlaLeuAlaThrGlyGlnLysAlaThrTyrSe 335
                                                                                           eThrProLysProSerLeu----IleLysAlaAlaLeulleAlaGlyAlaThrAspVa 295
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Publication No. US20020132335A1

GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: SHINOJO, TOMOKO
APPLICANT: SHINOJO, TOMOKO
APPLICANT: SHINOJO, TOMOKO
APPLICANT: SHINOJO, TOMOKO
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT APPLICATION NUMBER: 09/45,472
PRIOR APPLICATION NUMBER: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-10-06
SPIOR FILING DATE: 1999-10-06
SPIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SSEQ ID NO 5
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Matches:
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ORGANISM: Artificial Sequence
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APPLICANT: OMURA, SATOSHI
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APPLICANT: ISHIKAMA, UUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIUVKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPREMENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
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Db 6919665 CGGGTCAGTGTGCCGACGCCGTCGGGGCCCGCGTCACCGCGACGGGC 6919712  Qy 328 ThrGlyGlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIleSer 347  :: :: ::: ::: ::: ::: ::: ::: ::: :::		APPLICANT: IREANA, HARGO  APPLICANT: HORIKANA, UUN  APPLICANT: HORIKANA, HIROSHI  APPLICANT: SHIBA, TADAVOSHI  APPLICANT: SHIBA, TADAVOSHI  APPLICANT: HATTORI, MASAHIRA  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  FILE REFERENCE: 249-262  CURRENT APPLICATION NUMBER: US/10/156,761  CURRENT ILING DATE: 2002-05-29  CORRENT TILNG DATE: 2002-05-29  CORRENT APPLICATION NUMBER: 15 2001-204089	TE: 2001.05-30 ON WUMBER: UP 2001-27269 D NOS: 15109 D COMPACES avermitilis	OCATION: (1)(3417) -156-761-3306 ment Scores: 2.21e-25 Length: No.: 325.00 Matches: nt Similarity: 45.56\$ Conservat Local Similarity: 32.38\$ Mismatche Match: 14.38\$ Indels:	US-09-985-689A-4 (1-433) x US-10-156-761-3306 (1-3417)  Qy  18 GlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArg 37	Oy 78 Gly
Percent Similarity:       43.33%       Conservative:       56         Best Local Similarity:       28.97%       Mismatches:       153         Query Match:       14.51%       Indels:       68         DB:       14       31       31         US-09-985-689A-4 (1-433)       x US-10-156-761-1 (1-9025608)       37         QY       8 VallysalaaspValalaGlnAsnAsn       31         Db       6918813       GTCGAGGCGACATGGCCGAACACGCACAACGCCACAACGCCACAACGCCACAACGCCACAACGCCACAACGCACAACGCACAACGCCACAACGCCACAACGCACAACGCACAACGCACAACGCACAACA	Oy 18 GlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArg 37	6918975 78 6919035 93	CCTC 691920; CCTC 691920; CTCC 691926; CTCC 691926;	Db 6919263 GAGGAGCCGCCCTCTTCGTCGCGCGGGAAACACCGGTGCCCCTCCTCG 6919319  Qy 169 IleSerAlaProGlyThrAlaLySABnAlalleThrValGlyAlaThrGluAsnTyrArg 188	6919407 CCGCGCCACGGCACCACCCCTCAAGCCCGACCTCGCCGCGCGCTCGACTCGC 691946.  228 SerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyr 247  311	Db 6919866 GCGGAGCACCCCGACTGGACCGGCGCGCTCAAGGACGCTCATGTCCACGTCC 5919825  Qy 288 LeuileAlaGlyAlaThrAspValGlyLeuGlyTyrProAsnGlyAspGlnGlyTrpGly 307

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Gaps:
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
JAPLICANT: SARAKI, YOSHITUKI
TILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2001-06-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 5701
LENGTH: 3624
TYPE: DNA
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% A	228	Seralaargs	oAspSerSerPheTrp/   ::: :::  GGCACCGGCTAC	erSerLeuAlaProAspSerSerPheTrpAlaAsnTyrAsnSerLysTyr 247
ò	248		tAlaThrProlleVal	AlaglyAsnValAlaGlnLeu 267
qq	1249	ACCTCCATGAGCGGTACGTCGATGGCGACGCCCCATGTCGCGGGGGGTCGCCGCGCTCCTC	GGCGACGCCCCATGTCC	GCGGGGTCGCCGCTCCTC 1308
ò	268		GGlylleThrProLys	ProSerLeulleLysAlaAla 287
QQ	1309	GCCGAGCAGCACCCGACTGGACCGGCGCGCGCTCAAGGACGCGCTGATGTCCACGTCC	ceececececrcaac	GACGCGCTGATGTCCACGTCC 1368
ò	288	LeulleAlaGlyAl	GlyLeuGlyTyrPro	aThrAspValGlyLeuGlyTyrProAsnGlyAspGlnGlyTrpGly 307  :::
QQ	1369	GAGCAACTCGACGCCTCCGTATATCAGTTGGGGGCG	rcagirddddcg	GGT 1407
δ	308		uAsnValAlaTyrVali :	aTyrValAsnGluAlaThrAlaLeuAla 327
qq	1408	ĊĠĠĠĊAGTGTGCCGGACGCCGTCGGCGCC		cecercáccecec 1455
δχ	328	ThrGlyGlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIleSer	rPheGlnAlaGlnAlaG	GlyLysProLeuLysIleSer 347
a a	1456		crescecearsacsec	GATCGAĊĊGTCACGAAGACG 1515
ò	348		A	aSerTyrThrLeuValAsnAspLeu 367 :::
đ	1516	GTCACCTACTCCAACTCCTCCGACACGACGGTC	cacgácigec	GAGTTG 1554
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                                              ThrasnSerTrpGlyAlaProValAsnGlyAlaTyrThrAlaAsn-----SerArg 142
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Sequence 5701, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
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        |||| ::: |||| |------CTTATCCTTCAGCAAGCCCCGGGCACAGAACCT 1218
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APPLICANT: GHENG, Ni-ciang
APPLICANT: GHENG, Ni-ciang
APPLICANT: TANG, Gong-Li
TITLE OF INVENTION: Discrete Acyltransferases Ass
TITLE OF INVENTION: Synthases and Methods of Use
FILE REFERENCE: 564030-0021
CURRENT APPLICATION NUMBER: DCT/US02/08937
PRIOR APPLICATION NUMBER: DCT/US02/08937
PRIOR APPLICATION NUMBER: C60/278,935
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US 60/278,935
PRIOR FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 214
SOFTWARE: Patentin version 3.2
LENGTH: 135638
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// Publication No. US20030175888A1
// GENERAL INFORMATION:
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILLE REFRENCE: 10085.500-08
CURRENT APPLICATION NUMBER: US/9/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-327
NUMBER OF SEQ IDD NOS: 8481
SOFTWARE: PASESEQ for Windows Version 4.0
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                                                                                                                                  Length:
Matches:
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SEQ ID NO 1934
LENGTH: 1329
TYPE: DNA
ORGANISM: Bacillus licheniformis
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341.00
44.58%
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Best Local Similarity:
                                                                ; ORGANISM: Bacil
US-09-974-300-1934
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337 ATTAAGGGAGTTGAGTGGCCGTTGATAACAAGATAAGTACGGAATTAAGGTCATTAAT 396
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             TCAATAGCAGCTGGTACTGGAGCAGCAAGTAATGGCAAGTACAAGGGAATGGCTCCAGGA 276
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                                           AlaAsnLeuValPheGlnSerIleMet-----AspSerSerGlyGlyLeuGlyGlyLeu
                                                                   277 GCTAAGCTGGCGGGAATTAAGGTTCTAGGTGCCGATGGTTCTGGAAGCATATCTACTATA
                                                                                                ProSerAsnLeuAsnThrLeuPheSerGlnAlaTrpAsnAlaGlyAlaArgIleHisThr
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517 TATACAATCGGTTCTCCAGCAGCTGCAAGCTAATTACAGTTGGAGCCGTTGACAAG
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                                                                           US-10-090-624-15
, Sequence 15, Application US/10090624
, Publication No. US20020132335A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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1498 TAC------GGCTTCGAGAAGGTCGGCTACTACAACCCGACGCCGGAACCTGG 1545
1363 GCCACCCACACCTTCGACGTCAGGGGGCGACCTTCGTGACCGCCACCCTCTACTGGGAC 1422
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TTTGTCAATGGTAGG---AGTTATCCATACGATGGACCATGGACATGGAACTCATGTAGCT
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APPLICANT: TAKAKURA, Hikaru
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: MADADA, Kiyozo
APPLICANT: ARADA, Kiyozo
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFRENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: 09/445,472
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFWMARE: Patentin version 3:0
SEQ ID NOS:
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Publication No. US20020132335A1
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                                                                               8 ValLysAlaAspValAlaGlnAsnAsnTyrGlyLeuTyrGlyGlnGlyGlnValValAla
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                           US-09-985-689A-4 (1-433) x US-10-090-624-11 (1-1977)
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TGGGCGAACCATGACAGTAAATATGCATACATGGGTGGAACGTCCATGGCTACACCGATC
                                     GTTGCTGGAAACGTGGCACAGCTTCGTGAGCATTTTGTGAAAAAACAGAGGATCACACCA
                                                                                                                 300 ProAsnGlyAspGlnGlyTrpGlyArgValThrLeuAsnLysSerLeuAsnValAlaTyr
                        ValAlaGlyAsnValAlaGlnLeuArgGluHisPheIleLysAsnArgGlyIleThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10090624

| Publication No. US20020132335A1
| GENERAL INFORMATION:
| APPLICANT: TAKAKURA, Hikaru
| APPLICANT: TAKAKURA, Hikaru
| APPLICANT: SHIMOJO, TOMMOO
| APPLICANT: KHOSHITA, Mio.
| APPLICANT: ASADA, Kiyozo
| APPLICANT: ASADA, Kiyozo
| APPLICANT: ASADA, Kiyozo
| APPLICANT: ASADA, Kiyozo
| APPLICANT: ASADA, Kiyosio
| APPLICANT: ASADA, Kiyosio
| APPLICANT: MANATON: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
| TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
| TITLE OF INVENTION NUMBER: US/10/090,624
| CURRENT FILING DATE: 1997-06-10
| PRIOR APPLICATION NUMBER: 151969/1997
| PRIOR FILING DATE: 1997-06-10
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: PatentIn Version 3.0
| SEQ ID NO 11
| LENGTH: 1977
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Gaps:
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COTHER INFORMATION: Synthetic US-10-090-624-11
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Matches:
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Mismatches:
Indels:
Gaps:
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                                                           TYPE: DNA
ORGANISM: Bacillus sp. KSM-KP43
FEATURE:
                                                                                                                                                                 1.486-210
1987.50
94.33*
87.94*
  PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1305
                                                                                            , NAME/KEY: CDS
LOCATION: (1)..(1305)
, OTHER INFORMATION:
US-10-385-662-1
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Best Local Similarity:
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Pred. No.:
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sequence 1, Appli
JUSTIO-385-662-1
Sequence 1, Application US/10385662
Publication No. US20040002432A1
SEQUENCE 1, No. US20040002432A1
SEQUENCE 1. SATO. TOUROSHI
APPLICANT: SATO, TOUROSHI
APPLICANT: SATO, TOUROSHI
APPLICANT: SATO, TOURONI
APPLICANT: SAEKI, KATSUHIKO
APPLICANT: SAEKI, KATSUHIKO
APPLICANT: NOMURA, YOSHIFUMI
APPLICANT: NOMURA, MASAPUMI
TITLE OF INVENTION: ALKALINE PROCESSE
FILE REFERRNCE: 234938USO
CURRENT APPLICATION NUMBER: US/10/385,662
CURRENT APPLICATION NUMBER: US/202-081428
PRIOR PLING DATE: 2002-03-12
PRIOR PLING DATE: 2002-03-25
PRIOR PLING DATE: 2002-03-6-06
PRIOR APPLICATION NUMBER: JP 2002-104230
PRIOR APPLICATION NUMBER: JP 2002-104231
PRIOR APPLICATION NUMBER: JP 2002-104231
PRIOR APPLICATION NUMBER: JP 2002-304230
PRIOR APPLICATION NUMBER: JP 2002-304231
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                                  Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Capt2 1/USPTO spool/USO9985689/runat_31032004 161809_4271/app_query.fasta_1.3498
-Q=/Capt2 1/USPTO spool/USO9985689/runat_31032004 161809_4271/app_query.fasta_1.3498
-QB=Published Applications NA -QFMT=fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNITS=bite -GTRATT=1 -END=-1 -MATRIX=blosum62
-TRANS=humar40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRANS=humar40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXIEN=200000000 -USER=US09985689 @CGN 1 1 601 @runat_31033004 161809_4271
-NCPUS= -NO MMAAP -LARGEQUERY -NGS GCRES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TINEOOT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                 April 4, 2004, 08:10:21; Search time 327.248 Seconds (without alignments) 4948.852 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/USO6_NEW PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/USO6_PUBGOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/USO6_PUBGOMB.seq:*
6: /cgn2_6/prodata/1/pubpna/USO8_NEW PUB.seq:*
7: /cgn2_6/prodata/1/pubpna/USO8_NEW PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/USO8_NEW PUB.seq:*
9: /cgn2_6/prodata/1/pubpna/USO8_NEW PUB.seq:*
10: /cgn2_6/prodata/1/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/USO9_NEW PUB.seq:*
11: /cgn2_6/prodata/1/pubpna/USO9_NEW PUB.seq:*
12: /cgn2_6/prodata/1/pubpna/USO9_NEW PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/USO0_PUBCOMB.seq:*
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16: /cgn2_6/prodata/1/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/USO0_NEW PUB.seq:*
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12: /cgn2_6/prodata/1/pubpna/USO0_NEW PUB.seq:*
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2260
1 NDVARGIVKADVAQNNYGLY.....BVQAXNVPSGPQRFSLAIVH
                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                              OM protein - nucleic search, using frame plus p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2108 TCGGCGTACGTGGTCGCACGGGCGGGCAGACGGTCCGCACGGCCGCCGCGGTGCAG 2167
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GTCGACGACAAGGACAAGCTCGCCGAC 1507
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                                                                                                                                                                                                                                                                                                                                                           283 LeulleLysAlaAlaLeu-----IleAlaGlyAlaThrAspValGlyLeuGlyTyr 299
                                                                                                                                                                                                                                                                                                                                                                                                           300 ProAsnGlyAspGlnGlyTrpGlyArgValThrLeuAsnLysSerLeuAsnValAlaTyr 319
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                                              1367 Gredacaagergregecgagaaggeggreergrregecarededdddaaddaaddag
                                                                                      ValAspGluTyrValArgAsnAsnAspMetThrValLeuPheAlaAlaGlyAsnGluGly
1328 GGCATGGACACCGGAGACCGACCGCTGGAGGCGGCG----
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Search completed: April 4, 2004, 12:02:30 Job time: 90.4512 secs

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1100 GCGGCGCCCGGCGCGCGCGCGCGCGCGCGCCACGTCGCCTCGATCGCGGCG 1159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 GlyLeuTyrGlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ArgThrAsnAsnAlaSerAspProAsnGlyHisGlyThrHisValAlaGlySerValLeu
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces antibioticus
                                                                                                                                                                                                  REGISTRATION NUMBER: 40,949
REFRENCE/ DOCKET NUMBER: cunknown>
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFS: 202-721-820
TELEFAX: 202-721-825
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,340
FILING DATE: 28-Feb-2000
FLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P
NO: 1:
                                                                                                             APPLICATION NUMBER: 09/000,016
FILING DATE: January 30, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
Wordperfect 5.1
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IDENTIFICATION METHOD:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2809 base pairs
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IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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40.93$
28.98$
15.07$
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Best Local Similarity:
Query Match:
DB:
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HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE
ITS EXPRESSION PRODUCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GlnLysAlaThrTyrSerPheGlnAlaGlnAlaGlyLysProLeuLysIle 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 SerTyrProTyrAspAsnAsnTrpAspGlyArg------AsnAsnValGlu 399
222
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PheSerSerArgGly---AlaThrArgAspGlyArgIleLysProAspValThrAlaPro
                                   223 GlyThrPheileLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsn
                                                                                                                        1568 GGCGTGGACATCACGGCCGCCTCGGCGGAGGCAACGACATCGGCCAGGAGGTCGGTGAG
                                                                                                                                                                   243 TyrAsnSerLysTyrAlaTyrMetGlyGlyThrSerMetAlaThrProlleValAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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Patent No. 6361987
GENERAL INFORMATION:
APPLICANT: ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A
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CORRESPONDENCE ADDRESS:
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                                                                                                                          290 IlealaGlyAlaThrAspIleGlyLeuGlyTyrProSerGlyAsnGlnGlyTrpGlyArg 309
                                                                                                                                                                          310 ValThrLeuAspLysSerLeuAsnValAlaPheValAsnGluThrSerSerLeuSer--- 328
                                                                                                                                                                                                                                                                          337 PheThrAlaGlnSerGlyLysProLeuLysIleSerLeuValTrpSerAsp----- 353
                                                                                                                                                                                                                                                                                                                             354 -----AlaProAlaSer----ThrSerAlaSerValThrLeuValAsnAspLeuAsp 369
                                                                                                                                                                                                                                                                                                                                                                             370 LeuValileThrAlaProAsnGlyThrLysTyrValGlyAsnAspPheThrAlaProTyr 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------GluValGlnAlaTyrAsn 420
                         GlyThrSerMetAlaThrProIleValAlaGlyAsnValAlaGlnLeuArgGluHisPhe 272
                                                                                                                                                                                                                          -----ThrAsnGlnLysAlaThrTyrSer 336
                                                                                                                                          273 IleLysAsnArgGlyIleThrProLysProSerLeuLeuLysAlaAlaLeu-----
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Search completed: April 4, 2004, 01:12:51 Job time : 364.684 secs

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Matches:
Conservative:
                                                               US-09-514-340-1

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US-08-945-471-376C-4

US-08-945-471-8-7

US-09-945-918-1

US-09-945-918-15

US-09-966-921A-1

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| Sequence 5, Application US/09509814A
| Patent No. 637627
| GENERAL INFORMATION:
| APPLICANT: TAKAIWA, MITSUYOSHI
| APPLICANT: SAEKI, KATSUHISA
| APPLICANT: SAEKI, KATSUHISA
| APPLICANT: KUGOTA, HIROMI
| APPLICANT: KAGEYAMA, YASUSHI
| APPLICANT: KAGEYAMA, SHITSUW
| APPLICANT: KAGEYAMA, SHITSUW
| APPLICANT: NOWURA, MASARUMI
| TITLE OF INVENTION: ALKALINE PROTEASE
| FILE REFERENCE: 032-082-0676
| CURRENT PELING DATE: 2000-04-06
| PRIOR FILING DATE: 1998-10-07
| PRIOR FILING DATE: 1998-10-07
| PRIOR FILING DATE: 1998-10-07
| PRIOR FILING DATE: 1997-06-08
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NOS: 24
| SEQ ID NOS: 24
| SEQ ID NOS: 24
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       Percent Similarity:
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US-09-509-814A-5
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           Command line parameters:
-MODEL=frame+ p2n.model-DEV=xlh
-MODEL=frame+ p2n.model-DEV=xlh
-MODEL=frame+ p2n.model-DEV=xlh
-MODEL=frame+ p2n.model-DEV=xlh
-DE=ISSUGE PETER - TRANS=INSTER - I - MATRIX=blosum62 - TRANS=Inman40.cdi
-LOOPEXT=0 - UNITS=bits - GTRAT=1 - END=-1 - MATRIX=blosum62 - TRANS=Inman40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODE=LOCAL - OUTPMT=pct - NORA=sct - HEARSIZE=500 - MINLEN=0 - MAXLEN=200000000
-USER=US09985689 @CGN 1 1 142 @runat 31032004 161807 4184 - NCPU=6 - ICPU=3
-NO MAAP - LARGEQUERY - NGG SCORES=0 - WAIT - DSPELOCK=10 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - TRREADS=1 - XAAPOP=10 - LONGLOG
-FGAPEXT=7 - YGAPOP=10 - TRREADS=1 - XAAPOP=10 - KGAPEXT=0.5 - FGAPOP=6
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Sequence 41, Appli
Sequence 11, Appli
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Sequence 4, Appli
Sequence 34, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 6, Appli
                                                                                                                                                                                                                                            April 3, 2004, 23:50:44; Search time 63.5977 Seconds (without alignments) 3787.066 Million cell updates/sec
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1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                       - nucleic search, using frame_plus_p2n model
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US-09-509-814A-3
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US-08-894-818B-2
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US-09-844-818B-4
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US-08-844-818B-4
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Result No.

341 SerGlyLysProLeuLysIleSerLeuValTrpSerAspAlaProAlaSerThrSerAla :::	381 ValGIYASTASPPROTNIALAPPOTYTASPASHASHITYASPATATATATATATATATATATATATATATATATATATA	Db 1819 ANTGTATTTATTAATGCACCACAAAGCGGACGTATACAGTTAAGGGTACAGGCTTATAAC 1878  Qy 421 ValProGlnGlyProGlnAlaBheSerLeuAlaileValAsn 434  Db 1879 GTACCGGTTGGACCACAGACCTTCTGGTTGGCAATTGTGAAT 1920	ASOUR 509-814A-7; Sequence 7, Application US/09509814A; Sequence 7, Application US/09509814A; Patent No. 6376227; GENERAL INFORMATION: APPLICANT: TAKAIWA, MIKIO; APPLICANT: OKUDA, MIKSUXOSHI	APPLICANT: SAEKA, KAISUALSA ; APPLICANT: HIROMI ; APPLICANT: HIROMI ; APPLICANT: KAGEYAMA, YASUSHI ; APPLICANT: SHIKATA, SHITSUW	) AFPLICANT: NOMOUAN, MASARUMI ) TILLE OF INVENTION: ALKALINE PROTEASE ) FILE REFERENCE: 0327-0632-0PCT ) CURRENT APPLICATION VIONERE: US/09/509,814A ; CURRENT FILING DATE: 2000-04-06	; PRIOR APPLICATION NUMBER: PCT/JP98/04528 ; PRIOR FILING DATE: 1998-10-07 ; PRIOR APPLICATION NUMBER: UP 9-274570 ; PRIOR FILING DATE: 1997-06-08	) NUMBER OF SEQ ID NOS: 24 ) SOFTWARE: Patentin version 3.0 ) SEQ ID NO 7 LENGTH: 1923	; TYPE: DNA ; ORGANISM: Bacillus sp. ; FEATURE: ; NAME/KEY: CDS		2.48e-213 2141.00 ty: 97.93% arity: 93.55%	95.16% Indels: 4 Gaps: (1-434) x IR-09-509-814A-7 (1-1923)	1 ABINASVALA 1 ABINASVALA 1	21	4.1
Best Local Similarity:       93.55\$       Mismatches:       9         Query Match:       4       5.24\$       Indels:       0         DB:       4       Gaps:       0         US-09-985-689A-6 (1-434)       x US-09-509-814A-5 (1-1923)       0         QY       1 AshAsbValAlaArgGlyIleValLysAlaAspValAlaGlnSerSerTyrGlyLeuTyr       20         Db       619 AATGATGTTGCCGTGGAATTGTCAAAGCGGAAGTGGGCTCAGAGCTACGGGTTGTAT 678	ი — ი ი — ი	9 TCGAIGCATGAAGCCTICCGGGGAAAATTACTGCATTATATGCATTGGAACGAAT 1 ASRAlaasnAspProAsnGlyHisGlyThrHisValAlaglySerValLeuGlyAsnGly 1 ASRAlaasnAspProAsnGlyHisGlyThrHisValAlaglySerValLeuGlyAsnGly 1 ASRALAASAAGATGATGATGATGATGAGAAGGGCTGGCTGGCTCGTATTAGGAAACGGC	ThrserAshLysGlyMetAlaProGlnAlaAshLeuValPheGlnSerValMetAspSer   :::::	919 GGTGGGGGACTTGGAGGACTACCTTCGAATCTGCAAACCTTATTCAGCCAAGCATACAGT 978 121 AlaGlyAlaArglleHisThrAenSerTrpGlyAlaProValAenGlyAlaTyrThrThr 140	н б	161 GlyasnGluGlyProAsnGlyGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIle 180 	181 ThrValGlyAlaThrGluAsnLeuArgProSerPheGlySerTyrAlaAspAsnIleAsn 200	201 HisvalalacinPheSerSerArgGlyProThrLysAspGlyArgIleLysProAspVal 220 	221 MetalaproGlyThrPhelleLeuSeralaArgSerSerLeualaProAspSerSerPhe 240	241 TrpalaasnHisaspSerLysTyrAlaTyrMetGlyGlyThrSerMetAlaThrProile 260 	261 ValaladiyAsnValaladinLeuargGluHisPheIleLysAsnArgGlyIleThrPro 280 	281 LysproSerLeulysAlaAlaLeulleAladlyAlaThrAspIleGlyLeuGlyTyr 300 	301 ProSerGlyAsnGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAlaPhe 320    :::	321 ValasnGluThrSerSerLeuSerThrAsnGlnLysAlaThrTyrSerPheThrAlaGln 340 

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AlaGlyAlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyrThrThr 140
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               421 ValproglnGlyProGlnAlaPheSerLeuAlaileValAsn 434
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Matches:
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                                                                                                           Sequence 3, Application US/09509814A

patent No. 6376227

GENERAL INPORMATION:
APPLICANT: TAKNAWA, MIKIO
APPLICANT: ARKINAMA, MIKIO
APPLICANT: ARBERT, KATSUHUSA
APPLICANT: MITOMI, UNN
APPLICANT: HITOMI, UNN
APPLICANT: SHIKATA, SHITSUM
APPLICANT: SHIKATION: ALKALINE PROTEASE
TILE OF INVENTION: ALKALINE PROTEASE
TILE OF INVENTION: ALKALINE PROTEASE
TILE REFERENCE: 0327-0832-06-06
PRIOR FILING DATE: 1999-10-07
PRIOR APPLICATION NUMBER: DF 9-274570
PRIOR FILING DATE: 1997-06-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VEHENIN SEQ ID
MUMBER OF SEQ ID NOS: 24
SEQ ID NO 3
LENGTH: 1920
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97.70%
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; ORGANISM: Bacillus sp.
; FATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1920)
US-09-509-814A-3
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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798
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101 AsnGlyGlyLeuGlyGlyLeuProSerAsnValSerThrLeuPheSerGlnAlaTyrSer
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US-09-985-689A-6 (1-434) x US-08-873-479-41 (1-3003)
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APPLICATION NUMBER: US/08/873,479
FILING DATE: L2-UUN-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 5251.000-US
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION 1000-US
TELEFAX: 212-878-9655
                                                                                                                                  YSTEM: DOS
FastSEQ for Windows Version
No. 58917010 No. 5 Lexington Avenue
                                                          1.81e-210
2116.50
97.00%
92.17%
                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
IENGTH: 3003 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Genomic DNA
                                                                                                                            OPERATING SYSTEM:
SOFTWARE: FastSEC
 ADDRESSEE: No. STREET: 405 Lex. CITY: New York STATE: NY
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Best Local Similarity:
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APPLICANT: Lynne, Christianson
TITLE OF INVENTION: Nucleic Acids Encoding A Polypeptide
TITLE OF INVENTION: Having Protease Activity
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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US-08-873-479-41
Sequent 41, Application US/08873479
Patent No. 5891701
GENERAL INFORMATION:
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                                 GlyAsnGluGlyProAsnGlyGlyThrIleSerAlaFroGlyThrAlaLysAsnAlaIle
                                                                                  .947 GGAAATGAGGGACCAGGTAGCGGTACAATCAGTGCACCAGGAACAGCAAAAATGCGATT
                                                                                                                                                Thr ValGlyAlaThrGluAsnLeuArgProSerPheGlySerTyrAlaAspAsnIleAsn
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APPLICANT: TAXAKURA, Hikaru
APPLICANT: YAMAMOTO, Karsuhiko
APPLICANT: YAMAMOTO, Karsuhiko
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANTINASAWA, SUSUMU
APPL
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Patent No. 6261822
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1996
FILING DATE: 12-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/02253
FILING DATE: 12-DEC-1996
ATTORNEY/AGENT INFORMATION:
MANTE: BLOWAY, ROGET L.
REGISTRATION NUMBER: TAKAKURA=1
TELECOMMUNICATION INFORMATION:
TELEFRAN: (202) 628-5197
TELEFRAN: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTISS:
LENGTH: 1977 base pairs
TWDE: nucleic acid
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Mismatches:
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APPLICATION NUMBER: US/09/445,472
   CURRENT APPLICATION NUMBER: US/09/445.
CURRENT FILING DATE: 1999-12-06
PRIOR EPPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
                                                                                                                     NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 1977
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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450.50
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Best Local Similarity:
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US-09-445-472-11
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DB:
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1204 AAGGTGAAGACCGCCCTCATCGAGACCGCGCGACATAGTCGCCCCCAAGAAGATAGCGGAC 1263
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APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADO, INNOSHIN
TITLE OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA=6
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Patent No. 6358726
GENERAL INFORMATION
APPLICANT: TAKAKURA, HIKATU
APPLICANT: MORISHITA, Mio
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SHIMOJO, Tomoko
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-09-985-689A-6 (1-434) x US-09-445-472-2 (1-1236)
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APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
ITILE OF INVENTON: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAKURA-6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 1236
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Matches:
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Patent No. 6358726
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
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Conservative:
Mismatches:
Indels:
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                                                                            1.28e-32
406.50
44.22%
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Percent Similarity:

Best Local Similarity:

Query Match:

DB:
                                                        Alignment Scores:
Pred. No.:
JS-08-894-818B-4
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                             ulysileSerieuValTrpSerAspAjaProAlaSerThrSerAlaSerValThrLeuVa 365
                                                                                                                                                 365 lAsrAspLeuAspLeuVallleThrAlaProAsnGlyThrLysTyrValGlyAsnAspPh
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Fatent No. 6261822
GENERAL INFORMATION
APPLICANT: TANAKURA, Hikaru
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: ASADA, Kiyozo
APPLICANT: TSUMASWA, Susumu
APPLICANT: TSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMASWA, SUSUMAS
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STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTE: ED.C.
SIP: 20004
COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: TBM PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
CLEASSIFICATION DATA:
APPLICATION NUMBER: PCT/UP96/03253
FILING DATE: 10-DEC.1995
FRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/UP96/03253
FRICK APPLICATION NUMBER: 12-DEC.1995
FRICK APPLICATION NUMBER: 25.618
REFERENCY, ROGET I.
NAME: Browdy, ROGET I.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: 25.618
REFERENCE/DO
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                                                                     ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
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TELEFAX: (202) 737-3528	12 ValAlaGinSerSerTyrGly-LeuTyr 420 GTCTGCAGCTCAAGTTANGGCAACTTACGTTTG 24 nValValalaValAlaAspThrGlyLeuAspTh	ProAsnGlyHisGlyThrHisValAlaGlySerValLeuGl :::	Oy 112 TThrLeuPheserGlnAlaTyrSerAlaGlyAlaArg11eHisThrAsnSerTrpGlyAl 132	172 927 192 212 212 1014 232 1074
	Oy 385 eThralaProTyrAspAsnAsnTrpAspGlyArgAsnAsnValGluAsnValPheileAs 405	7 7575045	VENTION: EQUENCES EQUENCES NCE ADDRU A19 Seven Shington C. C. United () 04 ADABLE F( TEMP F()	"CAUSTIONING"

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APPLICANT: TAKAKURA, Hikaru
APPLICANT: MAISHITA, Mio
APPLICANT: MINISHITA, Mio
APPLICANT: MADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
TITLE OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERMOSTABLE
FILE REFERENCE: TAKAURA=6
CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33
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Patent No. 6358726
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44.22%
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COTHER INFORMATION: Synthetic
US-09-445-472-15
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Alignment Scores Pred. No.:	Score: Percent Similari		US-09-985-689A-6	Qy 12 Va	   Db 420 GT	Oy 24 nV	Db 480 CA	Qy 44 uA	ın	Oy 64			Qy 94 eG	Db 687 AA	Qy 112 rT	Db 747 GI	Oy 132 aF	Db 807 AA	Qy 152 mA	DD 867 CG	Qy 172 aF	Db 927 AC	Qy 192 eG	Db 964	Oy 212 sA	Db 1014 GC	Qy 232 rs	Db 1074 CP	Qy 252 yG	DD 1125 TC	Qy 272 eI	0DD 1180	Qy 289 U	1236 CF
Oy 345 uLysIleSerLeuValTrpSerAspAlaProAlaSerThrSerAlaSerValThrLeuVa 365	Db 1401 AACTGCCACATTATACTGGGACAATGCCAAT1431	Oy 365 lAsnAspLeuAspLeuValIleThrAlaProAsnGlyThrLysTyrValGlyAsnAspPh 385	Db 1432 -AGCGACCTTGATCTTTACCTCTACGATCCCAATGGAAACCAGGTTGACTACTTA 1487	385 eThralaProTyrAspasnAsnTrpAspGlyArgAsnAsnValGluAsnValPhelleAs	1488 CACCGCCTACTATGGATTCGAAAAGGTTGGTTATTA	Oy 405 nAlaProGinSerGlyThrTyrThrValGuValGinAlaTyrAsnValBroGinGlyPr 425  Dh 1524 CBACCCAATGAACATGAACATTAAAGTTGAAGTGAAGTGA	425 oGlnAlaPheSerLeuAlaIleValAsn 434	1575 TGCAAACTATCAAGTAGATGTGGTAAGT	RESULT 11	US-08-894-818B-6 ; Sequence 6, Application US/08894818B : Patent No. 6265822	GENERAL INFORMATION: ; APPLICANT: TAKAKURA, Hikaru	; APPLICANT: MORISHITA, Mio ; APPLICANT: YAMAMOTO, Katsuniko	APPLICANT: MITTA, Masanori	000000000000000000000000000000000000000	ILILE OF INVENTION: AFFERINGENCE ABLE FROIEASE GENES ; NUMBER OF SEQUENCES: 42 . CORDECAPANDENCE ANDERSO.	ADDRESSE: Browdy and Neimark CHARGESE: ALCANDER OF THE CHARGE CONTROL OF CANONING THE CHARGE OF	seventn street N.W., ste. ngton	SIAIE: D.C. COUNTRY: United States of America	COMPUTER READABLE FORM:	MEDIUM TIPE: Floppy disk COMPUTER: ISM PC COMPANIED COMPANIES: PC	CFEMALING SISIEM: PC-2005/MG-2005 SOFTWARE: Patentin Release #1.0, Version #1.30	CONNENT AFFILCATION DAIR:  ATTING DAME: US/08/894,818B	CLAINS DATE: 20-741-1990; CLASSIFICATION: 435-950; DDITOR ADDITORATE.	APPLICATION NUMBER: PCT/JP96/03253 FILING DATE: 07-NOV-1996	꿈통	FILING DATE: 12-DEC-1995	NAME: Browdy, Roger L. professional and a second a second and a second	REGISTARION NOMBER: 25,010 ; REFERENCE DOCKET NUMBER: 1AKAKURA=1 . TRIEDCOMMINICATION INFORMATION.	TELECOLOGY (202)   TELECOLOGY	0.4	LENGTH UNDER PAIRS  LENGTH IN THE PAIR PAIRS  TAYOR IN THE PAIR PAIR PAIR PAIR PAIR PAIR PAIR PAIR	STRANDENESS: double	MOLECULA TYPE: genomic DNA	0-10018-450-201

Alignment Pred. No. Score: Percent S Best Loca Query Mat. DB:	t Scores: .: Similarity: al Similarity: tch:	2.37e-32 405.50 45.11% 29.78% 18.02%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1977 134 69 165 1165	
86-60-SD	5-689A-6 (1-434	4) x US-08-894	4-818B-6 (1-1977)		
දු ද	12 ValAlaGlr	nSerSerTyrGly-	Y-LeuTyr	GlyGlnGlyGl 24	σ
3 8	24 nValValA	aValAlaAsp?	31vLeuAspThrGlvAr	AsnAspSerSerMetHisGl 44	
বুত	cs o	::: AATAATTGACI	]:::  ] 3GAATTGAC	:::      GCTTCTCATCC 52	<u> </u>
δ	44 uAlaPheA	neArgGlyLysileThral	alleTyrAla	ArgThrAsnAsnAlaAsn 63	
QD	522 AGATCTCC	: :	: : :       : : :	::: GTAGATTTTGTCAATGG 56	9
ò	64	AspPro	AsnGlyHisGlyThrHis	AspProAsnGlyHisGlyThrHisValAlaGlySerValLeuGl 78	
Db	567 TAGGAGTT	ATCCATACGATGAC	CATGGACATGGAACTCA	-th	9
δ	78 YASHGIYT	rSerAsn	LysGlyMetAla	snGlyThrSerAsnivsGlyMetAlaProGlnAlaAsnLeuValPh 94	=#
QQ	627 TACTGGAG	CAGCAAGTAATGG	CAAGTACAAGGGAATGGC	68	96
λ	94 eGlnSerVa	rValMetAsi	pSerAsnGlyGlyLeuGlyGlyLeuProS	11	2
qq	687 AATTAAGG	TTCTAGGTGCCGA	rggriciggaagcaratc	aattaaggitictaggigccgalggitictggaagcalatctactalaattaagggagitga 746	9
ò	112 rThrLeuPhe	neSerGlnAlaTyrSe	rSerAlaGlyAlaArgile	HisThrAsnSerTrpGlyAl 13	2
g	747 GTGGGCCG	TTGATAACAAAGA?	TGGGCCGTTGATAACAAGATAAGTACGGAATTAAGGT	80	90
ò	132 aProvalA	nGlyAl	aTyrThrThrAspSerArgAsnVa`	snValAspAspTyrValArgLysAs 152	22
QQ	807 AAGCCAGAG	GCTCCGACGGAAC	cagagetecgacggaacteceteagteaggeegteaacgeetuggga	98 292	9
ķ	152 nAspMetAl	aValLeuPheAl	aAlaGlyAsnGluGlyPro	SerAl 17	2
qu	867 CGGTATAG	ggraragrerecgreed	cecchacacceccc	TACACCGTCGGCTC 92	97
ò	172 aProGlyThrAl	hrAlaLysAsnAlaIleThrVa	alleThrValGlyAlaThrGluAe	nLeuArgProSerPh 19	2
Db	927 ACCGCCG	[ ]	-69 -69	96	23
ò	192 eGlySerT	rTyrAlaAspAsnIle    :::	eAsnHisValAlaGlnPhe	erArgGlyProThrLy 21	2
q	964	GTTGACAGCAA	-grrókcagcaacaacarcóccagcrrcca	dcaddddddddddd 10	013
à	212 sAspGlyArg	rglleLysProAs	ArgileLysProAspValMetAlaProGlyThrPheI	leLeuSerAlaArgSe 23	2
DÞ	1014 GGACGGAA	GGCTCAAGCCGGA	Agrogrodococogogor	rearaccccccccccc 10	173
ò	232 rSerLeuAl	aProAspS	spSerSerPheTrpAlaAsnHisAs	1 25	2
qq	1074 CAGC	. ₹	CATGGGCACCCCGATAAA	CCAGCATGGGCACCCCGATAACGACTACTACACCAAGGCCTC 112	124
ζò	252 yGlyThrS	SerMetAlaThrProIle	ValAlaGl	nLeuArgGluHisPh 27	7.5
q	1125 TGGAACCA	CACCCC	Grraced	CATCCTCCAG 11	179
ò	272 elleLysA	snArgGl	ProLy8P	rLeuLeuLysAlaAlaLe 28	68
ą a	1180GCCC	cacceaecregacc	ccceacaagaaakaaccec	cercarcaaaccacca 1	235
δλ	289 uileAlaGl	lyAlaThrAspIle	eGlyLeuGlyTyrPr   	30	80
qq	1236 CATAGTCG	cccccaaggadt	catagresececeaassasatasessaresectae	daracadd 128	280

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AlaTyrSerAlaGlyAlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAla 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 GlyThralaLysAsnAlalleThrValGlyAlaThrGluAsnLeuArgProSerPheGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 AspGlyArgileLysProAspValMetAlaProGlyThrPhelleLeuSerAlaArgSer 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerLeuAlaProAspSerSerPheTrpAlaAsnHisAspSerLysTyrAlaTyrMetGly 252
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Matches:
Conservative:
Mismatches:
Indels:
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                                        Streptomyces viridosporus
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360.50
43.38%
31.20%
                                                                                                                                                  NAME/KEY: CDS
LOCATION: 338...2539
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
ORIGINAL SOURCE:
ORGANISM: StreE
STRAIN: A-914
FEATURE:
                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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Patent No. 6143541

GENERAL INFORMATION:
APPLICANT: ALIA ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: ITS EXPRESSION PRODUCT
TITLE OF INVENTION: ITS EXPRESSION PRODUCT
TITLE OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AAGGCGC 1574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nAlaProGlnSerGlyThrTyrThrValGluValGlnAlaTyrAsnValProGlnGlyPr 425
                                                                                                                                                                                                                                                                                                                                             uLysileSerLeuValTrpSerAspAlaProAlaSerThrSerAlaSerValThrLeuVa 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 lAsnAspLeuAspLeuVallleThrAlaProAsnGlyThrLysTyrValGlyAsnAspPh 385
                                            ----AsnValAlaPheValAsnGluThrSe 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eThralaProTyrAspAsnAsnTrpAspGlyArgAsnAsnValGluAsnValPheIleAs
                                                                                                                                                                                               rSerLeuSerThrAsnGlnLysAlaThrTyrSerPheThrAlaGlnSerGlyLysProLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1524 CAACCCGACCGCGGAACCTGGACGGTCAAGGTCGTCAGCTAC--
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ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
ADDRESSEE: 2033 K Street, N.W., #800
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDEFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: January 30, 1998
CLIASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     퉘
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                                                yArgValThrLeuAspLysSerLeu---
                                                                                                                                                                                                                                                                                                                                                                                                          GACCGCCACCCTCTACTGGGAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACCGCCTACTAC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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|1334 GACACCGGAGCCGACCCGCTGGAGGGCGGCGGTCGACAAGCTGTCCGCCGAGAAGGGC 1393
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---CATCCGGACCTGAAGGGCCGGGTGACGACAAGAACTTCACCGCGCGCCCGGC 1111
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146
57
175
90
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Streptomyces viridosporus
STRAIN: A-914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ж
NO
NO
   REGISTRATION NUMBER: 40,949
                                                                        TELEPRONE: 202-721-8200
TELEFAX: 202-721-8200
TELEFAX: CONTROND >
INFORWATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2559 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
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IDENTIFICATION METHOD:

SEQUENCE DESCRIPTION: SEQ ID
US-09-514-340-3
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43.38%
31.20%
16.02%
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LOCATION: 338
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Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE
ITS EXPRESSION PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2071
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                                                                                                                                                                                                   1865 GGCGTCCAGCAGTGGCCGCACCCAACGAGCCGGTCACCAAGCAGCTGACCTACCGC 1924
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1655 GGCACGTCGATGGCGACCCCGCACGTCGCGGGCGCGGGGGCCCTCTGAAGCAGCAGCAG--- 1711
                                                                                                                                                                     309
                                                                                                                                                                                                                                                                              310 ValThrLeuAspLysSerLeuAsnValAlaPheValAsnGluThrSerSerLeuSer--- 328
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                                                                                                                                                                                                                                                                                                                                                                                                -----ThrAsnGlnLysAlaThrTyrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 IleAlaGlyAlaThrAspIleGlyLeuGlyTyrProSerGlyAsnGlnGlyTrpGlyArg
                                                   273 IlelysAsnArgGlyIleThrProLysProSerLeuLeuLysAlaAlaLeu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 PheThrAlaGlnSerGlyLysProLeuLysIleSerLeuValTrpSerAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COMPATIBLE
OPPERATING SYSTEM: MS-DOS
SOFTWARE: Nordperfect 5.1
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APPLICATION NUMBER: US/09/514,340
FILING DATE: 28-Feb-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/000,016
FILING DATE: January 30, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
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145
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90
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Matches:
Conservative:
Mismatches:
Indels:
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         COMPUTER KEADABLE SOWN:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Mordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NOMER: US/09/000,016
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 33,00
RIGG APPLICATION NUMBER:
FILING DATE: MARCHINE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ORGANISM: Streptomyces antibioticus
                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2809 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M
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43.16%
30.98%
15.80%
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IDENTIFICATION METHOD:
FEATURE:
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 COMPUTER READABLE FORM
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV
TITLE OF INVENTION: ITS EXPRESSION PRODUCT
NUMBER OF SEQUENCES: 7
CORRESSOUDENESS: 7
ADDRESSEE: Wenderoch, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
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1805 ATCCAGGCCGACAAGGCGCTCCAGCAGACCGTGATCGCCGACCCGGTCTCGGTGAGCTTC 1864
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                           -----GTCGACGACAAGGACAAGCTCGCCGACTTCTCCTCCACCAGCCCCGCCTCGGC 1534
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194 SerTyralaaspasnileasnHisValalaaGlnPheSerSerargGlyPro---ThrLys 212
                                                                                                                                                233 SerLeuAlaProAspSerSerPheTrpAlaAsnHisAspSerLysTyrAlaTyrMetGly 252
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                                                                          213 AspGlyArgIleLysProAspValMetAlaProGlyThrPhelleLeuSerAlaArgSer
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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APPLICANT: Akira ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE
ITS EXPRESSION PRODUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASDVAIAIAARGGIVIIEVAILYSALAASDVAIAIAGINSERSERTYRGIYLEUTYRGIY
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145
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CITY: Washington
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
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APPLICATION NUMBER: US/09/514,340
FILING DATE: 28-PED-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/000,016
FILING DATE: January 30, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: «Unknown»
TELEFPAX: 202-721-820
TELEFAX: «Unknown»
TELEX: «Unknown»
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Matches:
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LOCATION: 2540...2809
LDCATITION METHOD: P
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
2189 GTGACCGTCCGGCACATCGGCC 2210
                                                                                                      RESULT 15
US-09-514-340-1
; Sequence 1, Application US/09514340
; Patent No. 6361987
; GENERAL INFORMATION:
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: genomic
ORIGINAL SOURCE:
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GACACCCGGCTCGGCGGCACGTGGACGCGCGTACTCGGCGTACGTGGTCGCC---ACG 2128
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ATCCAGGCCGACAAGGGGGTCCAGCAGACGGTGATCGCCGACCCGGTCTCGGTGAGCTTC 1864
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                                                                                                                                                                                                                   1286 GCGCCCCCCCCAGGCCCCCACTCGTCAACATGAGCCTGGGC-------GGCATG 1333
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ValLeuPhe-----AlaAlaGlyAsnGluGlyProAsnGlyGlyThrIleSerAlaPro 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyThrAlaLysAsnAlaIleThrValGlyAlaThrGluAsnLeuArgProSerPheGly 193
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                                                                                                                                                                                                                                                                                        138 TyrihrinaspSerArgAsnValAspAspTyrValArgLys-----AsnAspMetAla 155
   MetAspSerAsnGlyGlyLeuGlyGlyLeuProSerAsnValSerThrLeuPheSerGln 117
                                                                                                                                            118 AlaTyrSerAlaGlyAlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAla 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 SerTyrAlaAspAsnIleAsnHisValAlaGlnPheSerSerArgGlyPro---ThrLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGlyArgIleLysProAspValMetAlaProGlyThrPheIleLeuSerAlaArgSer
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AlaproAlaSerThrSerAlaSerValThrLeuvalAshAspheuAsp 303	Qy 354	•

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APPLICANT: OXUDA, MITSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATO, TSUYOSHI
APPLICANT: SATIO, MAZUHINO
APPLICANT: SUMITOMO, NOBUTUKI
APPLICANT: SAEKI, KAZUHISA
APPLICANT: ROBAYASHI, TORRU
APPLICANT: NOWURA, WASAFUMI
ITLE OF INVENTION: ALKAINE POOLOGI
CURRENT APPLICATION: ALKAINE TOSTO
CURRENT APPLICATION NUMBER: US/10/385,662
CURRENT APPLICATION NUMBER: US/202-081428
PRIOR FILING DATE: 2003-03-12
PRIOR PELING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: UF 2002-165987
PRIOR PILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 2002-304230
PRIOR APPLICATION NUMBER: US 2002-304230
PRIOR APPLICATION NUMBER: US 2002-304231
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-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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| cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/NSO8_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/NSO8_NEW PUB.seq:*
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                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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Database

Result

Sequence 12, Appl Sequence 3, Appli Sequence 13, Appli Sequence 1, Appli Sequence 6, Appli

Sequence 18, Sequence 18

equence 14,

Sequence 12, 1 Sequence 9, Ag Sequence 13, Ap

Sequence 5, Appil Sequence 11, Appil Sequence 2, Appil Sequence 23, Appil Sequence 29, Appil Sequence 5, Appil Sequence 1, Appil Sequence 1, Appil Sequence 112429, Sequence 117, Appil Sequence 11, Appil Sequence 11, Appil Sequence 11, Appil Sequence 20, Appil

900

320

1080

360

380

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321 ValAsnGluThrSerSerLeuSerThrAsnGlnLysAlaThrTyrSerPheThrAlaGln 340
721 TGGGCGAACCATGACAGTAAATATGCATACATGGGTGGAACGTCCATGGCTACACCGATC 780
                                                                         Valalagiyasnvalalaginjeuarggiuhispheilelysasnarggiyilethrpro
                                                                                                                                301 ProSerGlyAsnGlnGlyTrpGlyArgValThrLeuAspLysSerLeuAsnValAlaPhe
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Sequence 11, Application US/10090624

Publication No. US2002013233511

GENERAL INFORMATION:

APPLICANT: TAKAURA, Hikaru

APPLICANT: SHIMOJO, Tomoko

APPLICANT: SAZO, IKUOSHIN

TILLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE

TILLE REFERENCE: TAKAKURA=6

CURRENT APPLICATION NUMBER: 09/445,472

PRIOR FILING DATE: 1999-12-06

PRIOR PILING DATE: 1997-06-10

PRIOR PILING DATE: 1997-06-10

PRIOR FILING DATE: 1997-06-10

MUMBER OF SEQ ID NOS: 33

SOOTWARE: PALENTIN VETSION 3.0

LENGTH 1977
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Matches:
Conservative:
Mismatches:
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Gaps:
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450.50
47.05%
31.36%
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Pred. No.:
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406
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                            Gaps:
                                                                        TYPE: DNA ORGANISM: Bacillus sp. KSM-KP43
                                                                                                                                                                                         7.45e-226
2143.00
97.93%
93.55%
95.24%
       PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENLIN VERSION 3.1
SEQ ID NO 1
LENGTH: 1305
                                                                                                FEATURE:

NAME/KEY: CDS

COCATION: (1)...(1305)

OTHER INFORMATION:

US-10-385-662-1
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Pred. No.:
Score:
Percent Similarity:
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Query Match:
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1369 CACACCTTCGACGTCAGCGCCCACCTTCGTGACCGCCACCCTCTACTGGGAC---- 1422
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                                                                                                                                                                                                                                         GluValGlnAlaTyrAsnValProGlnGlyProGlnAlaPheSerLeuAlaIleValAsn 434
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                                                                  -----Acegerceaeceacarceacircracercraceac
                                                                                                     375 ProAsnGlyThrLysTyrValGlyAsnAspPheThrAlaProTyrAspAsnAsnTrpAsp
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                                                                                                                                                                       GlyargasnasnvalGluasnvalPheIleasnalaProGlnSerGlyThrTyrThrVal
                                                                                                                             CCCAACGGGAACGAG---GTTGACTACTCCTACACCGCCTACTAC------
                                                                                                                                                                                                                                                                                                                        US-10-090-624-2

Sequence 2, Application US/10090624

Publication Vo. US20020132335A1

GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
APPLICANT: HORISHITA, Mico
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SHIMOJO, Tomoko
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
APPLICANT: ASADA, Kiyozo
CHERNY: APLICANT: NYENGHINOSTABLE
FILE REFERENCE: TAKAKURA-6
CURRENT APPLICATION NUMBER: US/10/090,624
CURRENT FILING DATE: 1999-12-06
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-06-10
NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 1236
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Matches:
Conservative:
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193 ATCGTCGATACGGGTATAGACGCGAAC---------CACCCGATCTGAAG 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LysProSerLeuLeuLysAlaAlaLeulleAlaGlyAlaThrAspileGly--- 297
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                                                                                133 ATAGGGGCCGATACCGTCTGGAACTCCCTCGGCTACGACGGAAGCGGTGTGGTGGTTGCC 492
                                                                                                                                                                                                              ---GlyMetAlaProGlnAlaAsnLeuValPheGlnSerValMet-----AspSerAsn 101
                                                                                                                                                                                                                                                                                                                                                             555 ATAGGGGTGGCCCCGGGGGGAAGCTCGTGGGGGCGTCAAGGTTCTCGGTGCCGACGGTTCG 714
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                                                                                                                   ValAlaAspThrGlyLeuAspThrGlyArgAsnAspSerSerMetHisGluAlaPheArg 47
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                                               ValLysAlaAspValAlaGlnSerSerTyrGlyLeuTyrGlyGlnGlyGlnValValAla
                                                                                                                                                                                      GlyLysIleThrAlaIleTyr---AlaLeuGlyArgThrAsnAsnAlaAsnAspProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 SerArgAsnValAspAspTyrValArgLysAsnAspMetAlaValLeuPheAlaAlaGly
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                                                                                                            aProvalAsnGlyAlaTyrThrThrAspSerArgAsnValAspAspTyrValArgLysAs 152
                                                      nAspMetAlaValLeuPheAlaAlaGlyAsnGluGlyProAsnGlyGlyThrIleSerAl
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Sequence 15, Application US/10090624

Sequence 15, Application US/10090624

Bedleation No. US2020132335A1

GENERAL INFORMATION:
APPLICANT: MOMISHITP, Mio
APPLICANT: SHIMOJO, Tomoko
APPLICANT: SADDA, Kiyozo
APPLICANT: KATO, Itmoshin
TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPERENCE: TAKAKURA=6
CURRENT APPLICATION NUMBER: 1202-03-06
FRIOR FILING DATE: 2002-03-06
PRIOR PELLING DATE: 1999-12-06
PRIOR PELLING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-16-10
NUMBER OF SEQ ID NOS: 33
SOCTUMES: Patentin version 3.0
SEQ ID NO 15
FURNATION OF 13
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APFLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
EINGTH: 3624
                                                                                                                                               ORGANISM: Streptomyces avermitilis
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; LOCATION: (1)..(3624)
US-10-156-761-5701
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Query Match:
DB:
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUNI
APPLICANT: HORIKAWA, JUNI
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARKI, YOSHIVUKI
APPLICANT: MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, UNN
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIRAY, TADAYOSHI
APPLICANT: ONUMER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
FRIOR APPLICATION NUMBER: UF 2001-272697
FRIOR PILING DATE: 2001-05-30
FRIOR FILING DATE: 2001-05-30
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              GTC-ACGCTGAACCTCGCGTCGACGGCGACCAACCCCAAGGGCGTCGCCGCTCCGTCGGG
                                                                    -----LysTyrValGlyAsnAspPheThrAlaProTyrAspAsnAsnTrpAspGlyAr
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                                                                                                                          1755 CTTCTTCAAGCTCGGCGCGACGAAGGTCACGGTCCCGGCG--
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Mismatches:
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APPLICANT: HORIKAWA, JUNA
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHRBA, TRAAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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ORGANISM: Streptomyces avermitilis
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Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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Best Local Similarity:
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8757 ---racaccaccardasocederacerceardecedecedecederecedederorgecedes
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                                                                                                                ### CAGGGCCCGCGTGACGGCGACGGCTGAAGCCGGAAGATCACCGCGCCCGGCGTCGAC
                                                                                                                                                                                   IleLeuSerAlaArgSerSerLeuAlaProAspSerSerPheTrpAlaAsnHisAspSer
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                                                                              ArgGlyProThrLys---AspGlyArglleLysProAspValMetAlaProGlyThrPhe
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; Retent No. US20020146721A1
; Retent No. US20020146721A1
; GENERAL INFORMATION:
APPLICANT: Clausen, Ib Groth
ITLE OF INVENTION: Methods For Monitoring Multiple Gene
ITLE OF INVENTION: Expression
FILE REFERENCE: 10085.300-45
; FILE REFERENCE: 2001-10-05
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
; RROR FILING DATE: 2000-10-06
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                                                  APPLICANT: SHEN, Benn APPLICANT: CHENG, Y1-Qiang APPLICANT: CHENG, Y1-Qiang APPLICANT: CHENG, Y1-Qiang APPLICANT: TANG, Gong-Li.

TITLE OF INVENTION: Discrete Acyltransferases Associated with Type I Polyketide TITLE OF INVENTION: Synthases and Methods of Use TITLE OF INVENTION: Synthases and Methods of Use CURRENT APPLICATION NUMBER: US/10/314,657

CURRENT APPLICATION NUMBER: US/10/314,657

CURRENT FILING DATE: 2002-12-09

PRIOR APPLICATION NUMBER: PG/20837

PRIOR APPLICATION NUMBER: US 60/278,935

PRIOR FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 214

SSD THARE: Patentin Version 3.2

SSD THARE: Patentin Version 3.2
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Matches:
Conservative:
Mismatches:
Indels:
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           Publication No. US20030175888A1
GENERAL INFORMATION:
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Best Local Similarity:
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                            Length:
Matches:
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337.50
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                    Alignment Scores:
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1219 GATGAAGTCAAACAGCTGCTAATGGACGGT---ACCGATTTATGGAAAGATCGCGATCCA 1275
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Sequence 5, Application US/10090624

Sequence 6, Application W. US20020132335A1

GENERAL INFORMATION:

APPLICANT: TAKAKURA, Hikaru

APPLICANT: SHIMOJO, Tomoko

APPLICANT: SHIMOJO, Tomoko

APPLICANT: SHIMOJO, Tomoko

APPLICANT: SHIMOJO, Tomoko

APPLICANT: SADA, Kiyozo

APPLICANT: SYSTEM FOR EXPRESSING HYPERTHERWOSTABLE

TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERWOSTABLE

CURRENT FILING DATE: 1097-06-06

PRIOR PLING DATE: 1099-12-06

PRIOR PLING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1997-06-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PALECTION VURSER: 151969/1997

SEQ ID NOS: 33

SEQ ID NOS: 33
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Conservative:
Mismatches:
Indels:
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ORGANISM: Artificial Sequence
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Query Match:
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λο O	164 GIYProAsnGIyGIyThrIleSerAlaProGIyThrAlaLysAsnAlaIleThrValGIy 183 	
Sy qq	184 AlaThrGluAsnLeuArgProSerPheGlySerTyrAlaAsp 197 	~B
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à d	300 TyrProSerGlyAsnGlnGlyTrpGlyArgValThrLeuAspLy8SerLeuAsnValAla 319 2041 TACACTGACTTGACCAAGGTCATGGTCTTGTTAACGTTAACGTAGTCCTGGGAAATC 2097	ă <i>6</i>
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NESOLUTION NO. US-10-084-846A-113
Sequence 113, Application US/10084846A
PUBLication No. US20040006026A1
GENERAL INFORMATION:
APPLICANT: WELTNAUER, GABRIELE
APPLICANT: MUBLENWEQ, AGNES
APPLICANT: TREFEZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
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56978 GACACGGCCGTACGCAAC-----GCCATGGCCTCCGGCGTCACCTTCGCCGTG 57025
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                                                      GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArgAsnAspSer
                                                                                                                                                                       SerMetHisGluAlaPheArgGlyLys1leThrAlalleTyr---AlaLeuGlyArgThr
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APPLICANT TRREZER, AXEL
APPLICANT BECHTHOLD, ANDREAS
APPLICANT BECHTHOLD, ANDREAS
TILE REFERENCE: 1974-005
CURRENT APPLICATION WUMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATENTIN OF: 3.2
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US-10-084-846A-1
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APPLICANT: WEITNAUER, GABRIELE
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2839 GACACGGCGTACGCAACGCCATGGCCTCCGGCGTCACCTTCGCCGTG 279.	Db 2791 GCGGCCGGCAACGAGTCGACGCCTCCACGAGGTCACCCGCACGCGTCACGAG 2735 Qy 179 AlalleThrValGlyAlaThrGluAenLeuArgProSerPheGlySerTyrAla 196	2734 GCCATCACGGTCGGCGACGACCAG	2674 TCCGTCCTC	217	Qy 237 AspSerSerPheTrpAlaAsnHisAspSerLysTyrAlaTyrMetGlyGlyThrSerMet 256	Qy 257 AlaThrProlleValAlaGlyAsnValAlaGlnLeuArgGluHisPhelleLysAsnArg 276	Qy 277 GlyileThrProLysProSerLeuLeuLysAlaAlaLeuIleAlaGlyAla 293	Qy 294 ThraspileGlyLeuGlyTyrProSerGlyAsnGlnGlyTrpGlyArgValThrLeuAsp 313	Qy 314 LysserLeuAsnValAlaPheValAsnGluThrSerSerLeuSerThrAsnGlnLysAla 333	334	Qy 354 AlaProAlaSerThrSerAlaSerValThrLeuValAsnAspLeuAsp 369	Qy 370 LeuVallleThrAlaProAsnGlyThrLysTyrValGlyAsnAspPheThrAlaProTyr 389 1: ::       ::	Qy 390 AspAsnAsnTrpAspGlyArgAsnAsnValGluAsnValPheIleAsnAlaProGln 408  2206GGCACCGGCGGCAGTTCGGACATCAACACCACGTACTCGGTGAACGCTCCTCG 2150	Oy 409SerGlyThrTyrThrValGluVal 416 	RESULT 15 19-09-927-827-33 18-8equence 33, Application US/09927827 19-Publication No. US20030036176A1	) GENERAL INFORMATION: ) APPLICANT: Bower, Stanley G. ) APPLICANT: Ramseier, Thomas M. ) IITLE OF INVENTION: Directed Genetic Engineering of Xanthomonas campestris	; FILE KEFEKENCE: 38-10/15824/8 ; CURRENT APPLICATION NUMBER: US/09/927,827 ; CURRENT FILING DATE: 2001-08-10 ; PRIOR APPLICATION NUMBER: US 60/279,493 ; PRIOR FILING DATE: 2001-03-28 ; NUMBER OF SEQ ID NOS: 69
370 LeuvallleThrAlaProAsnGlyThrLysTyrValGlyAsnAspPheThrAlaProTyr:::::::::::::::::::::::::::::::::::	CY 390 AspasnAsnTrpAspGlyArgAsnAsnValGluAsnValPheIleAsnAlaProGln 408  Db 57611GGCACCGGCGGCAGTTCGGACAACAACAACACCACGTTACTCGGTGAACGCTTCCTCG 57667	409SerGlyThrTyrThrValGluVal 416		-10-08 Sequen Public GENERA		TITLE OF INVENTION: AVILAMYCIN DERIVATIVES FILE REFERENCE: 1974-005 CURRENT APPLICATION NUMBER: US/10/084,846A CURRENT FILING DATE: 2003-02-25	PRIOR APPLICATION NUMBER: PCT/EFOL/09815 PRIOR FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: DE 101 09 166.4 PRIOR FILING DATE: 2001-02-25	NUMBER OF SEQ ID NOS: 120   STOWNER: Patentin Ver. 3.2   SEQ ID NO 2   LENGTH: 59816	; TYPE: DNA ; ORGANISM: Streptomyces viridochromogenes US-10-084-846A-2		ty: 29.20% Mismatches: 13.22% Indels: 15.22% Gaps:	-09-985-689A-6 (1-434) x US-10-084-846A-2 (1-59816) 21 GlyGlnGlyGlnValValAlaValAlaAspThrGlyLeuAspThrGlyArgAsnAspSer 40	Db 3169 GGGCAGGAAGGACGTCATCGACACCGGCGTCCGC 3128  Qy 41 SerMetHisGlualaPheArgGlyLysIleThrAlaIleTyrAlaLeuGlyArgThr 59  Dh 3127 American Amer	60 AsnAsnAlaAsnAspProAsnGYHisGJYHTHISValAlaGJYSerValLeuGJYAsn 79	Oy 80 GlyThrSerAsnLysGlyMetAlaProGlnAlaAsnLeuValPheGlnSerValMetAsp 99  3007 GCCTACGGCGTCGCCAAGAAGGCCAAGAAGATCGTAGGGGTCCGCGTGCTG 2960	Oy 100 SerasnGlyGlyLeuGlyGlyLeuProSerAsnValSerThrLeuPheSerGlnalaTyr 119	Qy 120 SerAlaGlyAlaArgIleHisThrAsnSerTrpGlyAlaProValAsnGlyAlaTyr 138

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2300 CIGGIAGIGGIGGCGGCCAACGAAGGCCIGGCCIGGCTGAIGCAGAACGACGGCGGC 2359
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, NAME/KEY: CDS
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Search completed: April 5, 2004, 02:55:48 Job time: 7399 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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Database

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ALLGAMENIO				cDNA, mRNA sequence.	BQ622771	BQ622771.1 GI:21649940	BST	Conidiobolus coronatus (Delacroixia coronata)		Eukaryota; Fungi; Zygomycota; Zygomycetes; Entomophthorales;	Ancylistaceae; Conidiobolus.	1 (bases 1 to 1605)
	RESULT 1 BQ622771	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE

Oy 178 ABINALAILETHIVALGIYALAITHIGH	1327GATATCTTAGCTCC 236 ProAspSerSerPheTrpAlaAe 1363TGGAAGGC 256 MetAlaThrProIleValAlad3 1408 ATGGCTTGCCCTCACATTGCTGG	RESULT 2  RESULT 2  RE3395336  LOCUS  LOCUS  BU395336  ACCESSION  RU395336  VERSION  RU395336  VERSION  RU395336  VERSION  RU395336  VERSION  RU395336  COURCE  SOURCE  Dictyostelium discoideum  ORGANISM  Dictyostelium discoideum  ORGANISM  ENATYOLE;  REFERENCE  Lobases 1 to 640)	AUTHORS Urushihara, H., Tanaka, Y., Kohar TITLE FULL length oDNA of Dictyostelli JOURNAL Unpublished (2002) COMMENT Contact: Tadasu Shini Center For Genetic Resource Inf National Institute of Genetics	1111 Yata, Mishima, Shizuoka 41 Tel: 81-559-81-6855 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp. Location/Qualifiers 1. 640 /organism="Dictyostell/mol_type="mRNA"   strain="AXA"     db xref="taxon 44689" /clone="dd818b16"	/sex="mat A" /dev stage="Slug s /clone_lib="Dictyo	Pred. No.:	Db 22 TTAAGAGGTAAAGGTCAGATATTGAGTA Qy 38AsnaspSer Db 82 TTCTTTCAGATTCAAAGTATCAAATAC
AUTHORS Freimoser, F.M., Screen, S., Hu, G. and St. Leger, R.J.  TITLE EST analysis of genes expressed by the zygomycete pathogen Conidiobolus coronatus during optimized secretion of proteins JOURNAL Unpublished (2002) COMMENT Contact: Freimoser F. M. Department of Entomology University of Maryland 4112 Plant Sciences Building, College Park, MD 20742, USA Tel: 301 405 16 13	FEATURES  Email: f134 92 90  Email: f134 92 90  Location/Qualifiers  1. 1605  1. 1605    mol type="mana"   monatus   monatus	nment Scores: No.: State Similarity: Local Similarity Match:	-09-985-889A-6 (1-4-4) A BC622/71 6 GlylleValLyshlaAspValA 718 GGTGTTGCTAAGGCTATTGCCG	Methis Me	63AshAspProAsnGlyHisGlyThrHisValAlaGlySerValLeuGlyAsn 79	982 599	. 4 4

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                 142 GTTGTAACTTATATT------ACTTACCATGACAATGAAGATTATGTAAAT 186
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 99
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 4198)

The FANTOM Consortium and the RIKEN Genome Exploration

Nature 409, 685-690 (2001) FANTOM Consortium. Functional annotation of

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II Team and

Group

Exploration Research

The RIKEN 20530913

Genome Res. 10 (11), 1757-1771 (2000)

a full-length mouse cDNA collection

Research

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Direct Submission

Submitted (16-UIL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegge: riken:go.jp, WEL:http://genome.gsc:riken:go.jp, Tel:81-45-503-9222, Presson
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transcription factor protease, site 1 (MGD|MGI:1927235,
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Oy 235 AlaProAspSerSerPheTrpAlaAsnHisAspSerLysTyrAlaTyrMetGlyGlyThr 254  1623 GTGAAAGGGGGTGC	Oy 315 SerLeuAsnValAlaPheValAsnGluThrSerSerLeuSerThrAsnGlnLysAlaThr 334  1827 GCTTATCAGATC	Db 1920 TCCCAGCCTATCTACTATGGAGGAATGCCAACAATGCTTAAT	RESULT 4 TA319G10P TA319G1	rivpanosoma.  REFERENCE 1 (bases 1 to 532)  AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  Melville,S.E., Rajandream,M.A. and Barrell,B.G.  TITLE Direct Submission  JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  nhissanger.ac.uk	COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREUSA74 GUTat 10.1) was mechanically sheared to give a tight size distribution ( 4 kb). The v+ i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
SVTKKAASWEGIAQGHIMITVASPAETELHSGAEHTSTVKLPIKVKIIPTPRSKRVL WDQYTHIRYPPSTFRRINGDHIMTWRDBMYDHIRSMOYFVETVAEF WDQYTHIRYPPSTFRENDHIMTRDBMYDHIRSMOYFVETVAEF TCFDATQYGTLLLVDSEEFYPPELBAKLRRDVDHGLSLVJFSDWYNTSVRKVKYEYDE NTRQWWMPDTGGANIPALBUSHVRNMGFSDGLYEGEFVLANHDMYXASGCSIAKFPE DGVYTTQTFRQGLEVVCRTATROCLSVRNMGFSDGLYARDHDMYXASGCSIAKFPE DGVYTTQTFRGADLALLQYTSVRTAFBSTGLAGRIRQRPPSGAGIAPPERGGHLHRYSKVLEA KLGDFKRPLPACPHLSWAKPQPINETAPSNLWKHQXLLSIDLDKVVLPNFRSNRPQV RPLEAGRANDIFGGINNGRYNOEVGGTIPVFAFLGAMVALAFFVVQISKAKSRPKR RPRAKRPQLAQQAHPARTPSV"  Anote="putative"  Note="putative"  ORIGIN  ORIGIN		QY 8 ValLysAlaAspValAlaGlnSerSerTyrGlyLeuTyrGlyGlnGlyGlnValValAla 27  1005 CTGCAGGCAGTGTGTGTGCAGATGGGATACACAGGTGCTAATGTGTTGT 1061  28 ValAlaAspThrGlyLeuAspThrGlyArgAsnAspSerSerMetHisGluAlaPheArg 47  Db 1062 GTTTTGATACTGGGCTCAGTGAGAAGGATCGGATTTTAAG 1103  QY 48 GlyLysIleThrAlaIleTyrAlaLeuGlyArgThrAsnAsnAsnAlaAsn		Db 1305 ATCCTAAAGAAGATGGACGTTCTCAACCTTAGCATCGTGGGCCCGACTTCATGGATCAT 1364  Qy 143 ArgAsnValAspAspTyrValArgLysAsnAspWetalaValLeuPheAlaAla 160  Db 1365 CCGTTTGTTGACAAGGTGTGGGAATTAACAGCTAACAATGTAATTATGGTTTCTGCTATT 1424  Qy 161 GlyAsnGluGlyProAsnGlyGlyThrIleSerAlaProGlyThrAlaLysAsnAlaIle 180  Db 1425 GGCAATGATGGACTTCTGAAGGCACTCTGAATAACCTGCTGATGAATGA	Oy 181 ThrValGlyAlaThrGluAsnLeuArgProSerPheGlySerTyrAlaAspAsn1leAsn 200  1485 GGAGTGGGCATTGACTTTGAAGATAACATC 1517  Db 1218 HisValAlaGlnPheSerSerArgGly

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21 AAAGITGTAACTTATATTACCACATCAACAAGCGACGATAGTGATAAAGTGGATGGTCAC
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                                                                                                                                                                                                                    /sex="mat A"
/dev_stage="Slug stage"
/clone_lib="Dictyostelium discoideum cDNA library,
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Unpublished (2002)
Contact: Tadasu Shin-i
Center Por Genetic Resource Information
Center Por Genetic Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                          /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
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Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

I (bases 1 to 594)
Urubnihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the slug stage
                                                                                                                                                                                                                                                                                               CATCCCAGTCAGAGCTTGTCCTCCCCCACGACGTTACTCAAATTATTCGTCCCGGTATAT
                                                                                                                                                                                                                                                                                valPheGlnSerValMetAspSerAsnGlyGlyLeuGly----
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61
28
68
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
    Location/Qualifiers
1. 532
/ organism="Trypanosoma brucei"
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Metarhizium anisopliae var. acridum
Metarhizium anisopliae var. acridum
Metarhizium anisopliae var. acridum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.

I (Abase 1 to 2141)
Freimoser,F.M., Screen,S., Baga,S., Hu,G and St. Leger,R.J.

EST analysis of genes expressed by two different insect pathogenic
fungi during optimized secretion of proteins
Contact: Freimoser F. M.
Department of Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA
Tel: 301 405 16 13
Fax: 301 314 92 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db.xref="taxon:92637" /clone lib="Metarhizium anisopliae sf. acridum ARSEF 324" /clone lib="Metarhizium anisopliae sf. acridum /note="Vector: Unizap; Metarhizium anisopliae sf. acridum was grwon on insect cuticle and chitin for 24 hours. A cDNA library was constructed in the unidirectional Lambda vector Unizap."
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909 AGCCGAAGCTACGGTGTTGCCAAAAATGCCAAGCTCTTTGCTGTCAAGGTTCTTGATGAC 850
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          Contig6 Metarhizium anisopliae sf. acridum ARSEF 324 Metarhizium anisopliae var. acridum cDNA, mRNA sequence.
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Location/Qualifiers
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BJ387574 DictyOstelium discoideum cDNA library, SF DictyOstelium discoideum cDNA library, SF DictyOstelium discoideum cDNA clone dds3al8 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 601)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Fill length chon, of Dictyostellum discoideum at the slug stage prull length chon, of Dictyostellum discoideum at the slug stage Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
National Institute of Genetics
Illi Yata, Mishima, Shizuoka 411-8540, Japan
Thel: 91-559-81-6856
                                                                                                                                  197 AspAsnIleAsnHisValAlaGlnPheSerSerArgGlyProThrLysAspGlyArgIle
                                                                                                                                                                                                                                                                                                                              237 AspSerSerPheTrpAlaAsnHisAspSerLysTyrAlaTyrMetGlyGlyThrSerMet
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258
47
741
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/clone="dds3a18"
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Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Dictyostellum discoideum
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BJ387574.1 GI:19296958
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Best Local Similarity:
Query Match:
DB:
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/organism="Trypanosoma bruce;"
/mol type="genomic DNA"
/strain="Trypanosoma bruce;"
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/clone="Species of Sheared DNA-8F2"
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/clone="Species of Sheared DNA-8F2"
/clone="Species of Genomic Research (TIGR), Rockville, MD.
Genomic DNA, isolated from a cloned population of
Trypanosoma bruce; (TREU227/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barell, Oxford University
Press, 1999)."
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UI-M-FWO-cby-d-23-0-UI.rl NH BMAP_FWO Mus musculus CDNA clone
UI-M-FWO Cby-d-23-0-UI.rl NH BMAP_FWO Mus musculus CDNA clone
URAGE:6816072 5', mRNA sequence.
CA320325
CA320325.1 GI:24538449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProAspSerSerPheTrpAlaAsnHisAspSerLysTyrAlaTyrMetGlyGlyThrSer 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 GCATCAGCAAAA--------CAATGTAAAGTGGTGGCCAAGCGGGGTTCATCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValLeuPheAlaAlaGlyAsnGluGlyProAsnGlyGlyThrIleSerAlaProGlyThr 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetalaThrProlleValAlaGlyAsnValAlaGlnLeuArgGluHisPhelleLys---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 IleLysProAspValMetAlaProGlyThrPheIleLeuSerAlaArgSerSerLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 AlaAspAsnIleAsnHisValAlaGlnPheSerSerArgGlyProThrLysAspGlyArg
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Query Match:
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CA320325
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Other GSSs: Sheared DNA-8F2.TR
Contact: Najib M. El-Sayed
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.ligr.org/tdb/mdb/tbdb/.
Seq primer: M13-Forward
Class: shotgun:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ552212 508 bp DNA linear GSS 22-JUN-1999 Sheared DNA-8F2.TF Sheared DNA Trypanosoma brucei genomic clone sheared DNA-8F2, genomic survey sequence.
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                                                                                                                                                      218 ProAspValMetAlaProGlyThrPheIleLeuSerAlaArgSerSerLeuAla----
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1 (bases 1 to 508)

El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fuj Gersard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J., Fraser,C. and Adams,M.

Determination of clone end sequences from Trypanosoma brucei 10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 ProSerLeuLeuLysAlaAlaLeulleAlaGlyAla-----
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                     US-09-985-689A-6 (1-434) x BJ387574 (1-601)
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AQ652212/c
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AUTHORS
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COMMENT
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us-09-985-689a-6.rst

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SM Zygosaccharomyces rouxii

Edwaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Zygosaccharomyces.

1 (bases 1 to 1002)

S Soucit.G.L., Aigle.M., Artiguenave,F., Blandin,G.,

Solotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,

Malpstuy,A., Neweglise,C., Ozler-Kalogeropoulos,O., Potier,S.,

Sautin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

FEBS Lett. 487 (1), 3-12 (2000)
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T3 end of clone AR0AA010H04 of library AR0AA from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.
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340 ATCCTAAAGAAGATGGACGTTCTCAACCTTAGCATCGGTGGGGCCCGACTTCATGGATCAT 399
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GATGATGGGCTAGGCCATGGCACATTCGTTGCAGGT---GTGATTGCCAGCATGAGGGAG 237
                                                                                                                                                                                                                                                                                                                143 ArgAsnValAspAspTyr-----ValArgiysAsnAspMetAlaValLeuPheAlaAla
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658 GTGAAAGGGGGCTGC------CGTGCACTCTCAGGGACC
                                                                                                                                  GlyLeuGlyGlyLeuProSerAsnValSerThrLeuPheSerGlnAlaTyrSerAlaGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1002)
de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Souciet, J.
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/dev_stage="embryole brain"
/dev_stage="embryole brain"
/dev_stage="embryole brain"
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Site_2: Not I; The library was constructed according
Bonaflo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a i% agarose
gel. First strand CDNA synthesis was primed with oligo-dr
primer containing a Not I site brack entropy as size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lows Brain Anatomy Project (BMAPP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mentell Health (NIMH), Hemin Chin, Ph.D.,
                                    Mus musculus nuouse nouse, Musses nuouse, Musses nuouse, Musses nuovo musculus nuouse, Chordata, Craniata, Vertebrata; Euteleostomi; Eukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus. (Bases 1 to 771)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1991)

Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be clone Distribution: MGC clone distribution information can be tound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
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